



Universidade Federal do Paraná  
Departamento de Zoologia  
Programa de Pós-Graduação em Ciências Biológicas  
Área de concentração em Entomologia



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## **Diversidade de Arctiinae (Lepidoptera: Erebidae) ao longo de um gradiente altitudinal na Serra do Mar do Paraná, Brasil**

Tese apresentada à Coordenação do Programa de Pós-Graduação em Ciências Biológicas, Área de Concentração em Entomologia, do Setor de Ciências Biológicas, da Universidade Federal do Paraná, como requisito parcial à obtenção do título de Doutor em Ciências Biológicas.

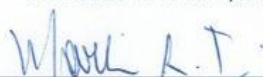
Orientador: Prof. Dr. Marcio Roberto Pie

**Curitiba**  
**Fevereiro, 2013**

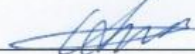
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"Diversidade de Arctiinae (Lepidoptera: Erebidæ) ao longo de um gradiente altitudinal na Serra do Mar do Paraná, Brasil"

Tese aprovada como requisito parcial para obtenção do grau de Doutor em Ciências, no Programa de Pós-Graduação em Ciências Biológicas, Área de Concentração em Entomologia, da Universidade Federal do Paraná, pela Comissão formada pelos professores:



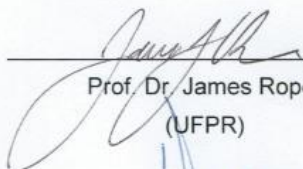
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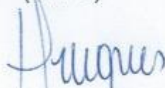
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Curitiba, 07 de fevereiro de 2013.

Dedico esta Tese a todas as pessoas que ensinam a pescar e não apenas dão o peixe.

## **Agradecimentos**

Gostaria de agradecer a todas as pessoas que me ajudaram ao longo desses quatro anos em que estive empenhado na árdua tarefa de produzir esta Tese, especificamente meu Pai (Lauro Zenker), minha mãe (Sirlei Moraes Zenker) e minha esposa (Tatiana Pineda Portella Zenker). Também quero manifestar o meu mais profundo agradecimento às pessoas que foram determinantes em minha carreira, em especial o Dr. Alexandre Specht (Embrapa Cerrados) , que acreditou no meu potencial, ao Prof. Dr. Marcio R. Pie (UFPR) pela oportunidade de orientação e conselhos e aos Professores Dra. Carla M. Penz e Dr. Philip J. DeVries (University of New Orleans) pela calorosa acolhida durante o período em que estive nos EUA, pela valiosa revisão de minha Tese e pela co-orientação.

Gostaria também de agradecer aos demais co-orientadores que contribuíram para a identificação dos espécimes de Arctiinae, Prof. Dr. José Augusto Teston (UFOP, Brasil) e Dr. Michel Laguerre (Institut Européen Chimie et Biologie, França) e ao Dr. Rodolphe Rougerie (Université de Rouen, França) pelo gerenciamento do projeto Lepidoptera of Serra do Mar junto ao Canadian Centre for DNA Barcoding.

Também agradeço à University of New Orleans pelo subsídio para a compra de um computador, ao Consortium for the Barcode of Life pela isenção de taxas para obtenção de sequências de código de barras de DNA, às agências brasileiras de fomento à pesquisa (CNPq e CAPES) pelas bolsas de estudo, às minha colegas Annie e Laura (University of New Orleans) e aos meu colegas do Laboratório de Dinâmica Evolutiva e Sistemas Complexos (UFPR) pela parceria e amizade. Por fim gostaria de agradecer aos habitantes da Estrada da Graciosa pelo auxílio para a realização do meu trabalho de campo.



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## Resumo

A subfamília Arctiinae (Lepidoptera: Erebidae) é um dos grupos de mariposas mais facilmente reconhecidos e carismáticos devido à sua coloração exuberante. Diversos aspectos relacionados com a interação inseto-planta, importância médica e agrícola e a utilização como indicadores de mudanças ambientais tem sido estudados nas mariposas desta subfamília, destacando a importância de estudos de diversidade para esse grupo. Padrões espaço-temporais de riqueza e abundância de arctíneos em gradientes altitudinais na América do Sul, utilizando coletas padronizadas, tem sido estudados somente ao longo da Cordilheira dos Andes, inexistindo estudos similares na Mata Atlântica. Considerando que este bioma é altamente ameaçado, tais padrões são essenciais para conhecer a riqueza de espécies, se uma determinada espécie é abundante ou rara em uma região/altitude, e o período de ocorrência dessa espécie. Dessa forma, o conhecimento desses padrões fornece importantes informações para a conservação e servem de base para diversos outros estudos. Padrões de diversidade de Arctiinae ao longo de um gradiente altitudinal de aproximadamente 1.000 s.n.m, na parte sul da maior área de Mata Atlântica contínua do Brasil, foram estudados por dois anos tendo como objetivos: (1) descrever os padrões de riqueza, abundância e diversidade encontrados; (2) correlacionar essas variáveis com a altitude; (3) avaliar a diversidade e a mudança na composição de espécies ao longo da altitude e do tempo; (4) comparar os resultados com outros estudos de diversidade para a tribo Arctiini no limite sul da Mata Atlântica, Pampa e Amazônia. Adicionalmente, uma biblioteca de código de barras de DNA foi construída com amostras de espécimes provenientes deste trabalho e a correspondência entre morfoespécies e espécies delimitadas pelo código de barras de DNA foi avaliada. As amostragens foram efetuadas entre fevereiro de 2010 e janeiro de 2012 na região da Serra da Graciosa (parte integrante da Serra do Mar), litoral paranaense. Foram selecionados 14 pontos de coleta em uma área de Floresta Ombrofila Densa com pouca ou nenhuma influência antrópica e variação altitudinal entre 7m e 927m. Para a descrição geral da assembléia de espécies foram utilizados dados totais (14 pontos de coleta), e para comparação entre pontos foram utilizados dados de nove pontos com maior amostragem. Desses nove pontos de coleta, quatro estão localizados na floresta Montana, dois na floresta Submontana e três na floresta de Terras Baixas. As coletas foram efetuadas mensalmente e simultaneamente com uma armadilha luminosa automática em cada ponto de coleta. As amostras foram triadas no laboratório e foi formada uma coleção de referência com os *singletons* e ao menos três exemplares de cada morfoespécie montados em alfinetes entomológicos; os demais exemplares foram acondicionados em envelopes entomológicos. Amostras de tecido, imagens digitais e dados taxonômicos e de coleta para aproximadamente todos os exemplares presentes na coleção de referência foram enviados ao *Canadian Centre for DNA Barcoding*, onde as sequências de código de barras de DNA foram geradas, e todas as informações inseridas em um banco de dados *on-line* vinculado ao projeto *Barcode of Life - BOLD Systems*. Ao todo foram obtidos 14026 exemplares pertencentes a 294 morfoespécies, em 224 amostragem. Apesar da riqueza ser maior os valores de alfa de Fisher e de riqueza rarefeita de espécies (medidas de diversidade) para Arctiinae são, em geral, menores em altitudes mais elevadas. Isso se deve ao fato da abundância ter sido muito maior nesse ambiente se comparado com locais de menor altitude. Para Arctiinae como um

todo houve uma correlação negativa não significativa entre os valores de alfa de Fisher para os nove locais com maior amostragem e altitude, porém houve uma correlação negativa e significativa entre os valores de riqueza rarefeita de espécies e altitude. Três espécies do gênero *Agylla* que ocorreram com mais de 1.000 exemplares influenciaram nas correlações entre os valores de diversidade e altitude em Lithosiini e em Arctiinae como um todo. Os estimadores de riqueza de espécies utilizados indicam que o esforço amostral total revelou entre 84,4% e 95,5% do total de espécies com hábitos noturnos para a área de amostragem. Comparativamente a área amostrada neste estudo apresenta valores de diversidade para a tribo Arctiini muito superiores aos observados no limite sul da Mata Atlântica, Pampa e Amazônia. Isso se deve, provavelmente, à grande variação altitudinal na Serra da Graciosa. Em relação à composição da comunidade foi possível perceber uma mudança gradual ao longo dos três níveis altitudinais (Floresta de Terras Baixas, Submontana e Montana). Os padrões de sazonalidade encontrados sugerem que a diversidade é maior durante o período mais quente do ano em Floresta Montana, e durante o período mais frio em Floresta Submontana e de Terras Baixas. Durante a estação mais quente a composição da comunidade é diferente nos três níveis altitudinais, mas não durante a estação fria quando não há diferença entre Floresta de Terras Baixas e Submontana. A composição de espécies da tribo Arctiini observada neste estudo é diferente da observada no limite sul da Mata Atlântica e Pampa. Das 1117 amostras de arctíneos enviadas ao *Canadian Centre for DNA Barcoding* foi possível obter 1100 sequências de código de barras de DNA, sendo 1058 do tamanho padrão (658 pb) e apenas duas sequências com menos de 600 pb. O sucesso na amplificação e a alta qualidade das sequências obtidas podem ser atribuídos ao tipo de armadilha empregada na qual foi utilizado etanol 97% como meio de fixação. As 1100 sequências de código de barras de DNA compreenderam 290 das 294 morfoespécies obtidas nas amostragens. Essas informações e mais um total de 2117 imagens de exemplares de Arctiinae em vista dorsal e ventral coletados neste estudo estão disponíveis na *Internet* através de um banco de dados vinculado ao BOLD. A correspondência entre morfoespécies e espécies delimitadas pelo código de barras de DNA (i.e. ~ 65%) pode ser considerada relativamente alta, pois poucas sequências por espécies foram obtidas e a avaliação da morfologia foi superficial, considerando-se apenas a aparência externa do inseto. Da mesma forma que em estudos anteriores, casos de dimorfismo sexual e erros de identificação morfológica foram revelados pelo código de barras de DNA. Também houve casos em que o código de barras de DNA não foi capaz de distinguir espécies morfológicas e casos de espécies que necessitam estudos morfológicos mais aprofundados. Pelo menos 102 espécies de Arctiinae, identificadas ao nível de espécie, em que houve correspondência entre a identificação morfológica e pelo código de barras de DNA, podem ser identificadas através da biblioteca de códigos de barras de DNA do BOLD.

**Palavras chave:** Lepidoptera, diversidade, DNA barcoding, conservação

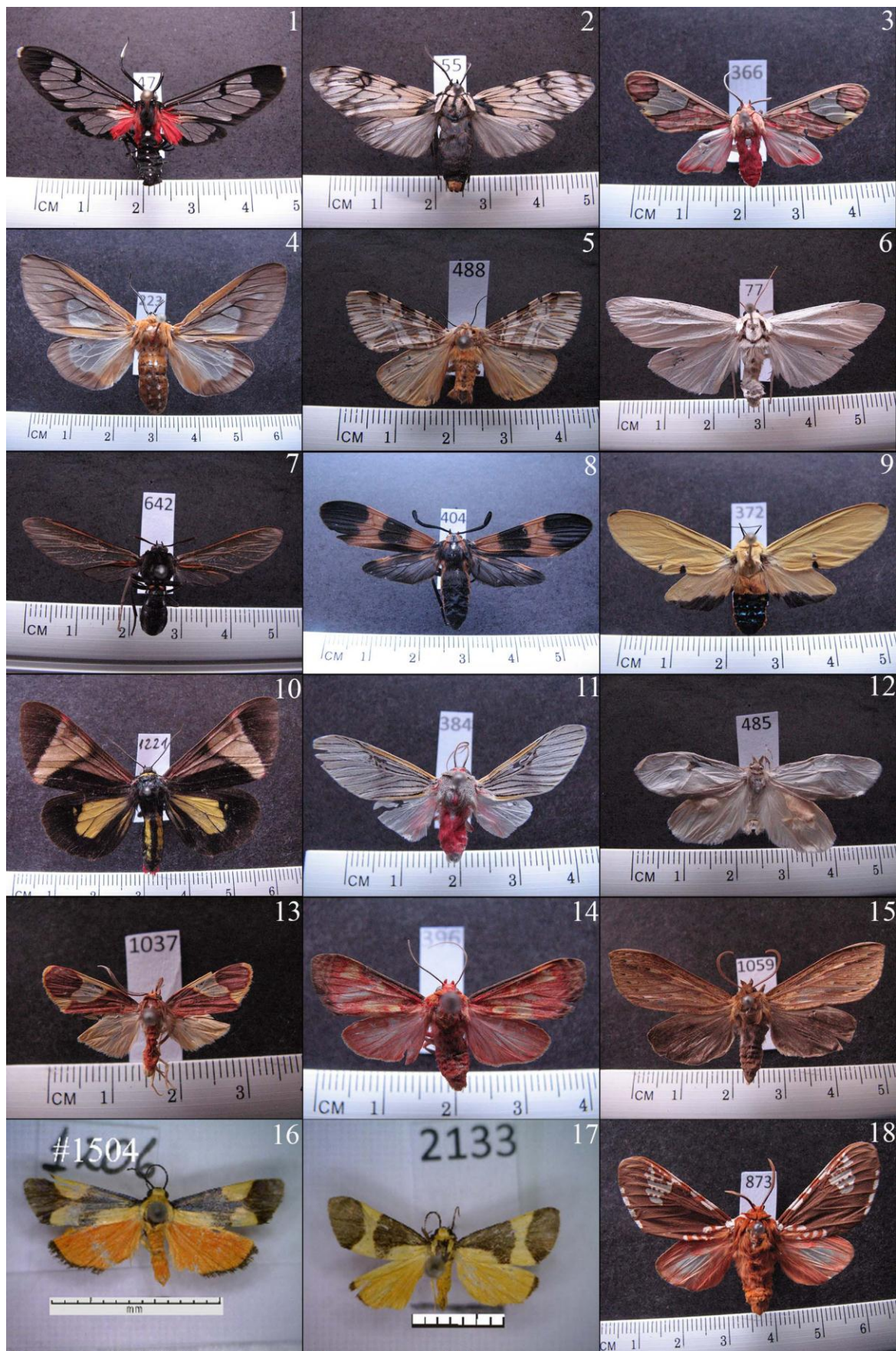
## Abstract

Moths of the subfamily Arctiinae (Lepidoptera: Erebidae) are among the most charismatic and promptly recognizable moths because their remarkable color patterns. Several studies have addressed topics such as insect-plant relationships, medical and agricultural relevance and the use of arctiins as environmental changes indicators, highlighting the importance of biodiversity surveys with this taxon. Spatiotemporal patterns of richness and abundance of arctiine along elevational gradients in South America, using standardized collections, have been studied only in the Andes mountains, whereas no study has been undertaken in the Atlantic Forest of Brazil to date. Considering that this biome is highly threatened, such patterns are essential to determine true species richness, whether a given species is abundant or rare in a region/elevation, and its period of activity. Therefore, these patterns are essential information to improve conservation efforts and can be used as the baseline for future studies. I studied diversity patterns of Arctiinae along an elevational gradient with near 1,000m a.s.l., located in the southern part of the largest continue patch of Atlantic Forest of Brazil, for two years aiming to: (1) describe the richness, abundance and diversity patterns found; (2) correlate these variables with elevation; (3) test whether diversity and species composition change along elevation and time; (4) compare the results with other biodiversity studies of the tribe Arctiini from the southern edge of the Atlantic Forest, Pampa and Amazon. Additionally, a library of DNA barcodes was assembled with samples obtained in this study and the correspondence between morphospecies and species delimited by DNA barcoding was evaluated. Sampling area is part of the *Serra do Mar* mountains and is located in the region of *Serra da Graciosa*. Fourteen sites in the *Floresta Ombrófila Densa* forest type with little or no disturbance and elevational range within 7 m and 927 m were sampled, from February 2010 to January 2012. Total data set (14 sampling sites) were used for community description, and comparisons between elevations were made using the data of nine sites where sampling effort was higher. Four of these nine sampling sites are located in Montane forest, two in Submontane forest and three in the Lowland forest. One automatic light trap was run in each sampling site once a month. Samples were sorted in the laboratory and a reference collection was assembled with the singletons and at least three pinned specimens of each morphospecies; the remaining specimens were kept in entomological envelopes. Tissue samples, digital images and taxonomy and collection data of near all specimens in the reference collection were submitted to Canadian Centre for DNA Barcoding, where DNA barcode sequences were generated, and all the information uploaded in the on-line database of the project Barcode of Life – BOLD Systems. A total of 14026 specimens of 294 species were obtained from 224 samples. Although arctiine species richness is higher in high elevations, Fisher's alpha and rarefied species richness (diversity measures) are usually lower in high elevations. This is because abundance is much higher in high elevations when compared to lower elevations. For arctiine as a whole there was a negative but not significant correlation between Fisher's alpha values of the nine sites with higher sampling effort and elevation, and a negative and significant correlation between rarefied species richness and elevation. Three species in the genus *Agylla* were extremely abundant, with more than 1,000 specimens each, and influenced the correlations between diversity measures and elevation in Lithosiini and Arctiinae as a whole. Species richness estimators revealed that between 84.4%

and 95.5% of the species with nocturnal habits in the sampling area were sampled. When compared to sites located in the southern edge of the Atlantic forest, Pampa and Amazon diversity is much higher in the *Serra da Graciosa*, and this might be explained by the steep elevational variation at this location. The results indicated a gradual change in community composition along the three elevations (Lowland, Submontane and Montane forests). The seasonality patterns suggested that diversity is higher during the hottest months of the year in Montane forest and during the coldest months in Submontane and Lowland forests. Species composition was different in the three elevations during the hottest months, but not during the coldest ones when there was no difference between Lowland and Submontane. Furthermore, species composition in the *Serra da Graciosa* is different from that observed in the southern edge of the Atlantic Forest and Pampa. It was possible to obtain 1100 barcode sequences, from the 1117 samples of arctiins submitted to Canadian Centre for DNA Barcoding; 1058 sequences were 658 bp long (standard DNA barcode sequence length) and only two sequences were shorter than 600 bp. The sequences amplification success and high quality might be attributed to the use of ethanol 97% as killing agent in the light traps. From the 294 species obtained in the collections, and the 1100 barcode sequences, it was possible to obtain barcode sequences for 290 species. All these information and a total of 2117 digital images in dorsal and ventral view of arctiine specimens obtained during the course of this study are available through the Internet in the BOLD database. The correspondence between morphospecies and species revealed by DNA barcoding (i.e. ~ 65%) can be considered high because we superficially analyzed the external morphology of the specimens and few sequences per species were available. Similarly to previous studies it was possible to verify cases of sexual dimorphism, and cases of species incorrectly discriminated by morphology. Additionally, in some cases DNA barcoding was ineffective to discriminate between clearly morphologically delimited species, and further morphological studies are needed in some species. It is possible to use the library of DNA barcodes of BOLD website to identify at least 102 entities identified to species level where DNA barcoding and morphology were in agreement.

**Key words:** Lepidoptera, diversity, DNA barcoding, conservation







Exêmplos de espécimes coletados neste estudo/Examples of specimens collected in this study: 1- *Erruca cardinale* (Euchromiina); 2- *Theages leucophaea* (Ctenuchina); 3- *Neonerita dorsipuncta* (Phegopterina); 4- *Sthenognatha gentilis* (Pericopina); 5- *Isia alcumena* (Artiina); 6- *Agylla* sp. JAT01 (Lithosiini); 7- *Sarosa* sp. ML01(Euchromiina); 8- *Correbia lycoides* (Ctenuchina); 9- *Viviennea superba* (Phaegopterina); 10- *Dysschema fantasma* (Pericopina); 11- *Idalus lineosus* (Phaegopterina); 12- *Agylla polysemata* (Lithosiini); 13- *Trichromia* sp. JAT02 (Phegopterina); 14- *Melese* sp. JAT01 (Phaegopterina); 15- *Arctiinae* sp. JAT24 (Phaegopterina); 16- *Illice cryptopygra* (Lithosiini); 17- *Illice ditrigona* (Lithosiini); 17- *Rhipha subflammans* (Phaegopterina).

## Chapter 1: Tiger moth diversity along an elevational gradient in Brazilian Atlantic Forest

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**Abstract:** Here we describe Arctiinae diversity along an elevational gradient in the Brazilian Atlantic Forest and test whether diversity changes from the sea level to almost 1000m a.s.l. We sampled 14 sites inside a preserved patch of forest, plus one site in the edge in the Southern coast of Brazil for two consecutive years. We sampled 14026 specimens in 294 species. Elevation and diversity, measured as species richness and Fisher's alpha, were independent of each other, but not when we used rarefied species richness as a diversity measure. Diversity declined with increased altitude in Lithosiini but not in Arctiini, but we found a significant positive correlation between altitude and dominance for Lithosiini due to three highly abundant *Agylla* species. Proportional abundance of Lithosiini was positively correlated with altitude that was driven by *Agylla* species alone, while the remaining Lithosiini correlated negatively with altitude. When compared to other biodiversity studies of the tribe Arctiini in different Brazilian biomes, the results suggest that diversity in our sampling area is higher than in the southern portion of the Atlantic Forest and eastern Amazon of Brazil.

**Key words:** Altitude, insect conservation, Mata Atlântica, Amazônia, Amazon, Pampa, Arctiidae.

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### 1. Introduction

Invertebrates and especially insects have been used extensively for environmental monitoring (e.g. Spellerberg, 1993; McGeoch, 1998; Hodkinson & Jackson, 2005), and to evaluate diversity patterns along different environmental gradients (e.g. DeVries *et al.*, 1997; Uehara-Prado *et al.*, 2009; Longino & Colwell, 2011). Nevertheless, the absence of basic ecological information for most terrestrial arthropods in the tropics is a major impediment to rapidly developing practical recommendations for conservation of rainforest ecosystems

(Basset *et al.*, 2004). In this context, moths have been particularly challenging for tropical biodiversity researchers.

Moths in the subfamily Arctiinae are often brightly colored and have larvae known to feed on toxic host plants, from where they acquire pyrrolizidine alkaloids (Weller *et al.*, 1999), which function as defenses against predation (e.g. Eisner & Eisner, 1991). The Arctiinae is distributed worldwide with approximately 11,000 described species grouped in three major lineages (i.e. Arctiini, Lithosiini and Syntomini) (Jacobson & Weller, 2002), and now placed within the highly speciose Noctuoidea as a clade of Erebidae (Zahiri, *et al.*, 2011; Zahiri, *et al.*, 2012). Of the approximately two thousand species of Arctiinae moths in Brazil (Brown and Freitas 1999), 1193 species occur in the Atlantic Forest, and represent ca. 60% and 20 % of the estimated Brazilian and Neotropical faunas, respectively (Ferro & Mello, 2011).

Arctiine diversity has been studied along a variety of environmental gradients especially in montane forests of Ecuador, Costa Rica, and Borneo (Hilt, 2005, Hilt & Fiedler, 2005, 2006, Noske *et al.*, 2008, Schulze *et al.*, 2001; Brehm, 2007, Sussenbach, 2003, Fiedler *et al.*, 2008, Beck *et al.*, 2011). However, little is known about their diversity along different gradients in eastern South America. The Serra do Mar is a mountain range extending along the coast of Brazil and, as part of the Atlantic Forest, is highly threatened by human pressure (Morelato & Haddad, 2000). Prior to Portuguese colonization the Atlantic Forest occupied 17.6% or 1.5 million km<sup>2</sup> of the Brazilian territory, a large portion of coastal land with approximately 29° latitudinal range, extending from northeast to south. However, Ribeiro *et al.* (2009) estimated that only 16% to 11.4 % of the original area remains, mainly in small fragments. Even so, the Atlantic Forest has one of the highest endemism rates in the world, underscoring its importance as a high priority conservation hotspot (Myers *et al.*, 2000; Brummit & Lughadha, 2003).

Based on museum specimens and published lists Ferro and Mello (2011) examined patterns of Arctiinae diversity in the Brazilian Atlantic Forest. They found a correlation between diversity and altitude, among other environmental variables. Although museum collections are valuable sources for estimating spatial and temporal species distributions, such records may have a patchy spatial coverage, often with some areas better sampled than others (Graham *et al.*, 2004). Studies of insect diversity with standardized sampling efforts along elevational gradients in the Atlantic Forest are scarce (but see Lazzari *et al.*, 2005 for Aphidae, Carneiro, 2012 for Hesperidae and Gonçalves *et al.*, 2012 for bees). Relatively unbiased sampling is essential for monitoring biotic elevational range shifts and lowland

attrition due to climate change since elevational temperature gradients are more pronounced than latitudinal gradients (Colwell *et al.*, 2008, Forister *et al.*, 2010). Given that arctiines are the most sensitive predictors of variation in North American Lepidoptera species richness (Summerville *et al.*, 2004), documentation of altitudinal diversity patterns may be especially useful for evaluating the Brazilian Atlantic Forest. Finally, arctiine species richness and composition may vary significantly among different mountain regions (Brehm, 2009), suggesting that identification of montane distributional patterns having distinct geological histories constitutes one of the baselines for large scale biogeographical studies.

Here we describe community diversity patterns of arctiine moths along an elevational transect of approximately 1000 meters in a patch of Atlantic Forest in southern Brazil. We also compare our results to a larger elevational gradient in the Ecuadorian montane rainforest, and to other studies that employed similar sampling techniques in Southern Brazil and Amazon region. We aimed to answer three questions: (1) Are elevation and diversity correlated in the sampling sites, and does this pattern vary between the different taxa within Arctiinae? (2) Does species composition vary with the altitude? (3) What is the species richness estimation for the study area, and is it higher than in the other regions?

## **2. Material and Methods**

### **2.1 Study area**

The study area is in the mountain region of Serra do Mar situated in southern Brazil, Paraná State (Fig. 1A). We used a State Road (PR-410 – Estrada da Graciosa) (Fig. 1B) as a transect through Serra da Graciosa (which is located within Serra do Mar) in order to access the sampling sites along a regional elevational gradient. We selected 14 sites with altitude between 7 and 927 m (Table 1, Fig. 1B). As the main focus of our work was to compare diversity along the elevational gradient rather than successional gradient, selected sites were mainly in the understory. However, to represent microhabitat variation, at least one small clearing site was sampled for each vegetation type, except for the sampling sites located between 200 and 434m; additionally we selected one human disturbed site in the upper part of the transect (Table 1). Although Arctiinae diversity can vary along vegetation succession (Hilt & Fiedler, 2005; Hilt & Fiedler, 2006), it is unlikely that this affected our sampling because understory and small clearing sites were inside a large section of primary forest, and no clearing sites were larger than 1000 m<sup>2</sup>. Furthermore, since traps were positioned near the forest edge (see distances from forest in Table 1), the small clearings might best considered

as edge habitats. For descriptive purposes the term small clearing is used throughout the text and tables.

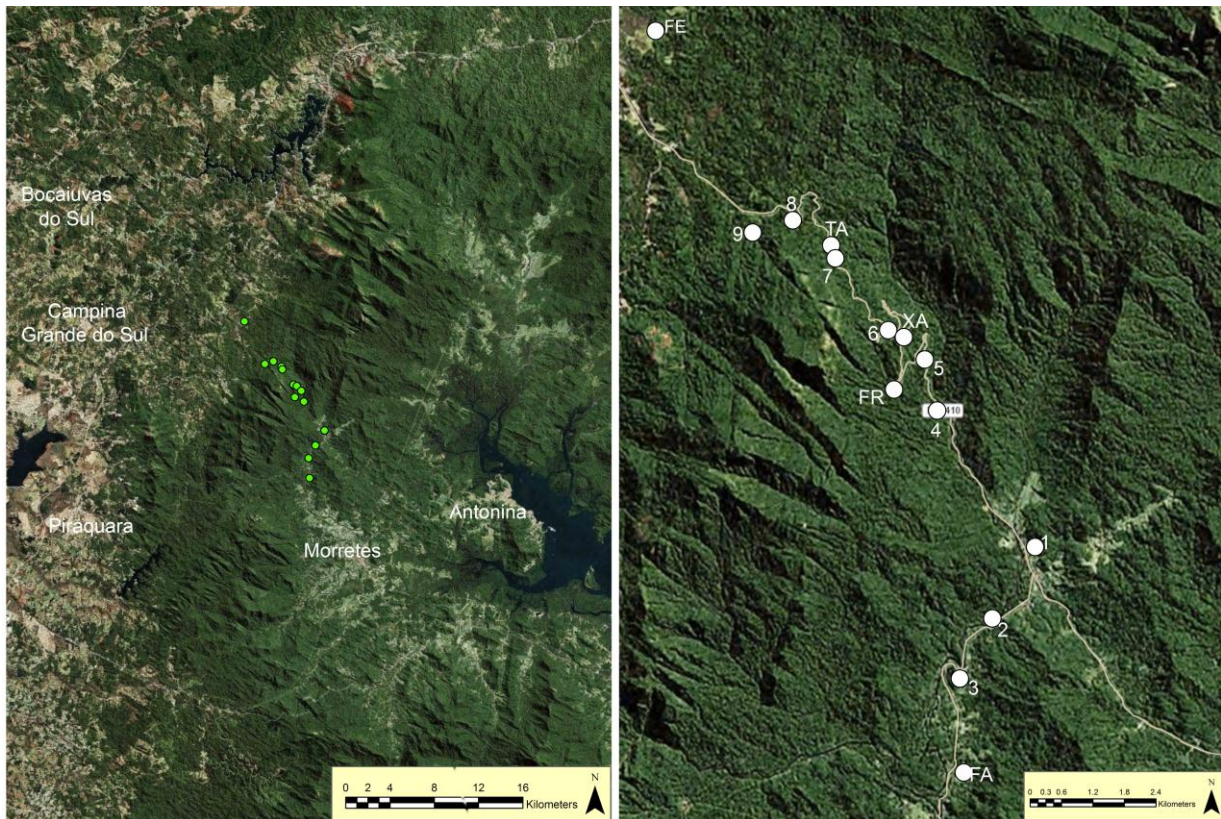
**Table 1** Sampling sites with details about location, vegetation structure, light trap distance from forest and level of disturbance. Sites number 1-9 have 20-24 sampling nights, and sites identified by letters have 1-14 sampling nights (see Table 2). LF: Lowland Forest, SF: Submontane Forest, MF: Montane Forest.

| Site | Altitude | Latitude (s) | Longitude (w) | Habitat characteristics | Distance from forest | Disturbance      |
|------|----------|--------------|---------------|-------------------------|----------------------|------------------|
| 1    | 7m       | 25°23'6.72"  | 48°51'39.65"  | LF Small clearing       | 10m                  | Moderate         |
| 2    | 15m      | 25°23'29.02" | 48°51'39.89"  | LF Understory           | -                    | Low              |
| FA   | 47m      | 25°25'9.43"  | 48°52'22.17"  | LF Understory           | -                    | Low              |
| 3    | 72m      | 25°23'59.47" | 48°52'17.54"  | LF Small clearing       | 25m                  | Moderate         |
| 4    | 200m     | 25°21'49.09" | 48°52'35.89"  | SF Understory           | -                    | Low              |
| 5    | 300m     | 25°21'18.47" | 48°52'44.49"  | SF Understory           | -                    | Low              |
| FR   | 393m     | 25°21'36.45" | 48°53'3.12"   | SF Understory           | -                    | Low              |
| XA   | 434m     | 25°21'17.62" | 48°52'59.52"  | SF Understory           | -                    | Low              |
| 6    | 579m     | 25°21'2.83"  | 48°53'8.96"   | MF Small clearing       | 28m                  | Moderate         |
| 7    | 700m     | 25°20'24.51" | 48°53'40.87"  | MF Understory           | -                    | Low              |
| TA   | 737m     | 25°20'16.38" | 48°53'42.74"  | MF Understory           | -                    | Low              |
| FE   | 850m     | 25°18'16.72" | 48°55'31.07"  | MF Clean Field          | 27m                  | Moderate to high |
| 8    | 873m     | 25°20'2.39"  | 48°54'6.88"   | MF Understory           | -                    | Low              |
| 9    | 927m     | 25°20'9.62"  | 48°54'31.04"  | MF Small clearing       | 23m                  | Moderate         |

The classification of vegetation in the study area varies among authors according to elevation; e.g. lowland forest: 0 – 30 m a.s.l. (Veloso *et al.*, 1991) or 0 – 20 m a.s.l. (Roderjan *et al.*, 2002). Because an extensive study of vegetation structure was beyond the scope of this study we used vegetation structure and physiognomy to establish gradient categories specific to our area. We identified three different vegetation types: lowland forest (between 7 and 72 m), submontane forest (between 200 and 434 m), and montane forest (between 579 and 927 m). Sites with 20-24 sampling nights (1-9) are numbered sequentially according to elevation, and sites with < 20 sampling nights are identified by letters corresponding to sampling site names (Table 1). Temperatures can fall below freezing between April and September in our study area. Nonetheless, for low and high elevation sites data from the last 40 years indicates mean monthly values for temperature and precipitation as: 59 m, 16.6 to 24.7 °C, and precipitation 78.7 to 300 mm; 930 m, 13.1 to 20.5 °C, and precipitation 71.6 to 193.1 mm (IAPAR, 2012).

## 2.2 Trap design and sampling procedure

Although there was no difference between automatic and manual sampling of arctiine moths in a Costa Rican study (Brehm & Axmacher, 2006), our study used only automatic traps for two reasons. First, automatic light traps allowed all traps to be run simultaneously, which is advantageous for the analyses employed here. Second, automatic light traps reduces collector bias and maximizes sampling when manpower is limited. The traps (model Pennsylvania; Frost, 1957) consisted of a white cloth funnel connected to a metallic frame equipped with a Sylvania 20W UV fluorescent tube, model W20T12. The tube emitted light at 356 nm (see details at [www.sylvania.com](http://www.sylvania.com)). We attached a 2 L plastic bucket to the base of the funnel filled with 90% alcohol (Specht & Corseuil, 2002; Teston & Corseuil, 2004). Details of the trap design are in Appendix 1I.



**Figure 1.** A) Study area in Serra do Mar mountains (Paraná State, Brazil) and nearby localities. B) Road used as a transect (PR-410 Estrada da Graciosa) and sampling sites in Serra da Graciosa. See Table 1 for altitudes.

One light trap was positioned in each sampling site with an average distance of 1.23 km between each trap, where minimum and maximum distances between contiguous sites ranged from 0.24 and 3.88 Km. To maximize sampling from canopy and understory (e.g., Schulze *et al.*, 2001; Brehm, 2007), traps were positioned 3 m from the ground. Sampling

occurred monthly from February 2010 to January 2012 when traps were run simultaneously at most sites from sunset to dawn (see Table 2 for details). To avoid possible bias effects of moonlight and meteorological factors (Yela & Holyoak, 1997, McGeachie, 1998), sampling was restricted from first quarter to third quarter moon periods, preferably during new moon, and during nights with air temperature equal or higher than 10 °C.

### 2.3 Sorting and taxonomic assignment

Representative specimens (at least three, when available) of each species/morphospecies were pinned for visual identification of wing and body color patterns; the remaining specimens were identified by comparison to the pinned specimens and stored in envelopes. All specimens were deposited at Laboratório de Dinâmica Evolutiva e Sistemas Complexos, Universidade Federal do Paraná, Curitiba-PR, Brazil. Images and identifications of all pinned specimens can be assessed at the Barcode of Life Database, [www.boldsystems.org](http://www.boldsystems.org), under the project “Lepidoptera of Serra do Mar”.

Species included in the Arctiini were identified by Dr. José Augusto Teston, based on the Brazilian collections cited in Teston and Corseuil (2002, 2003a, b). Arctiini species identified at the genus level were assigned to five subtribes according to references cited in Teston and Corseuil (2002). When genus level identification was not possible, species were assigned to subtribes based on external morphology and color pattern. Lithosiini species were identified by Dr. Michel Laguerre based on the collections of the Natural History Museum (London) and Muséum National d'Histoire Naturelle (Paris); systematic classification followed Jacobson and Weller (2002), Zahiri, *et al.*, (2011); Zahiri, *et al.*, (2012). Due to the lack of a stable subtribal classification for neotropical Lithosiini, species were assigned only to tribe.

### 2.4 Community description

Overall community diversity was described with a rank abundance plot, and species accumulation curves were used to show species richness and abundance for tribes, subtribes, and the complete dataset (see Colwell & Coddington, 1994; Chazdon *et al.*, 1998). We used descriptive statistics to characterize the proportion of taxa among sampling sites and, the Berger-Parker dominance index to test the relationships between richness, abundance and elevation with Spearman rank correlations followed by Bonferroni correction of the P values. We used cluster analysis based on Bray-Curtis distance to compare community similarity among sampling sites.

## 2.5 Fisher's alpha of the log series

We used Fisher's alpha of the log series and its 95% confidence intervals to describe alpha diversity along the elevational transect. Fisher's alpha provides a robust description of community diversity, even when the log series distribution is not the best descriptor of the underlying species abundance pattern (Magurran 2004). Values of Fisher's alpha for nine individual sampling sites with 20-24 sampling nights were calculated for Arctiinae and the main subordinate taxa. We correlated Fisher's alpha with elevation, species richness and abundance using Spearman rank correlation coefficients with P values adjusted by sequential Bonferroni correction. The log-series distribution was fitted with the program Species Diversity and Richness (Henderson and Seaby 1998). Values of Fisher's alpha for the log series and its 95% confidence intervals were calculated using R (R Development Core Team, 2012).

## 2.6 Rarefaction

To compare species richness among site we used rarefaction based upon 10,000 re-samples of the data. We used an individual rarefaction curve based for site 6 (mid-elevation) to test if species richness of the assemblage varied with elevation. Rarefaction curve for site 6 and its 95% confidence intervals were generated using EcoSim Professional Ver. 1.2d (Entsminger, 2012). We also calculated rarefied species number at different levels of abundance (see results section, Table 6). Rarefied species numbers allows direct comparisons between sampling sites based on the number of individuals for any sample size provided it is equal to or smaller than the smallest sample in the pooled data (Gotelli & Colwell, 2001; Hayek & Buzas, 1997), and provides an expected diversity measure independent of sample size. To test for any relationships between rarefied species number and elevation we used Spearman rank correlation coefficient with P values adjusted with sequential Bonferroni correction. Rarefied species number and its 95% confidence intervals were calculated using R.

## 2.7 Species richness estimators

The number of unrecorded species for the study area was estimated using seven common non parametric species richness estimators, i.e. Jackknife 1, Jackknife 2, Chao 1, Chao 2, Abundance Coverage Estimator (ACE), Incidence Coverage Estimator (ICE), Bootstrap, and Michaelis Menten Model (MMM). We used the decision framework



elaborated by Brose & Martinez (2004) to determine which estimator is most accurate for highly mobile animals. All estimations were calculated using the package EstimateS ver. 8.2.0 (Colwell, 2012).

### 3. Results

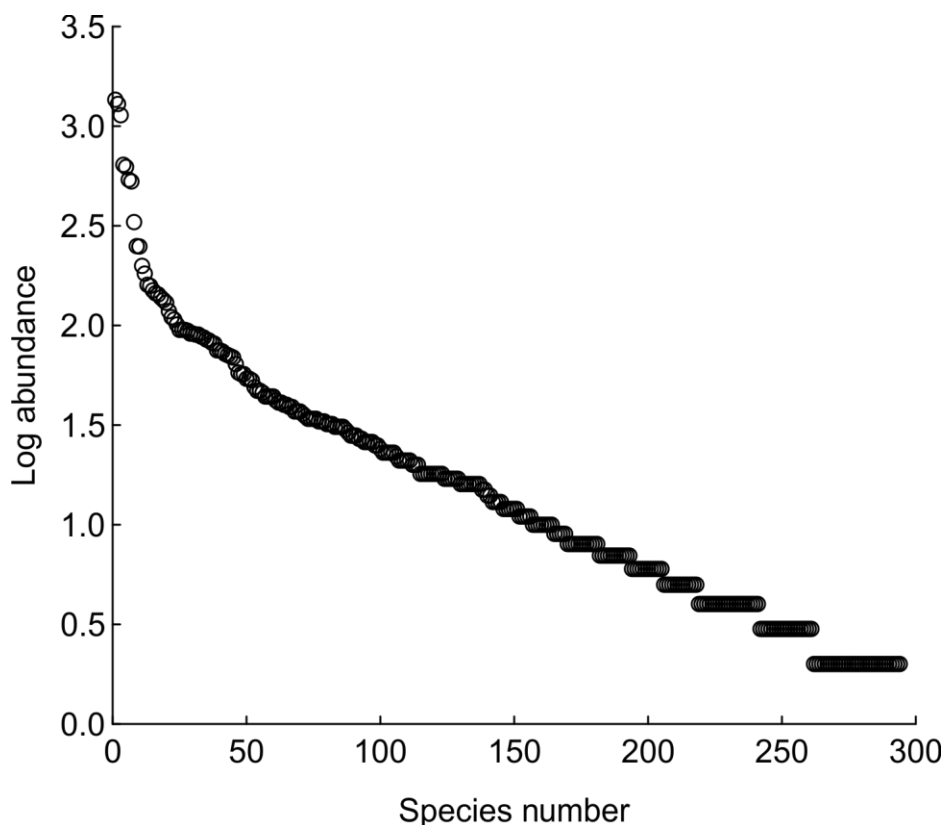
We sampled a total of 14026 specimens of 294 species in the 14 sites (Table 2). A species list with abundance data organized by tribes and subtribes is found in Appendix 2I. We were able to identify 53.4% of the individuals to species, 33.7% to genus and 12.9% to subtribe, including two Lithosiini morphospecies. Nine sites had 20 to 24 sampling nights, and these constitute the core of the data used in the analyses. Sampling effort in the remaining five sites varied between one and 14 nights, and these were used exclusively to estimate total species richness and to compute the species accumulation curves. Five species (*Cosmosoma plutona*, *Dinia* spJAT01, *Epidesma* spJAT01, *Demolis albicostata* and *Dysschema neda*) recorded only from excluded sites were omitted in comparisons between sampling sites.

**Table 2.** Species richness (S) and abundance (N) per site, and number of sampling nights from February 2010 to January 2012.

| Sites | Sampling nights | Arctiinae |     |
|-------|-----------------|-----------|-----|
|       |                 | (N)       | (S) |
| 1     | 20              | 434       | 109 |
| 2     | 23              | 501       | 98  |
| FA    | 1               | 34        | 22  |
| 3     | 24              | 862       | 153 |
| 4     | 23              | 1337      | 149 |
| 5     | 23              | 1316      | 142 |
| FR    | 1               | 55        | 12  |
| XA    | 5               | 368       | 92  |
| 6     | 23              | 3377      | 191 |
| 7     | 20              | 2168      | 157 |
| TA    | 2               | 35        | 15  |
| FE    | 14              | 181       | 63  |
| 8     | 23              | 1305      | 115 |
| 9     | 22              | 2053      | 129 |
| TOTAL | 224             | 14026     | 294 |

### 3.1 Richness, abundance and dominance

The community was well described by a log-normal distribution ( $\chi^2 = 132$ ,  $P = 0.2329$ ), with mean 3.77 and variance 2.64. The rank abundance distribution (Fig. 2) shows that species are relatively well distributed among abundance categories, with species with 10 or less individuals account for less than 50% of the sample (i.e. 48.64%). Five Lithosiini species (*Agylla* spJAT1, *Agylla* spJAT2, *Agylla* spJAT3, *Agylla* spJAT09 and *Agylla polysemata*) each had more than five hundred individuals, and represented 34.4% and 83% of Arctiinae and Lithosiini abundance. Elevation and dominance were correlated in Arctiinae and Lithosiini, although this correlation was supported only in Lithosiini after P correction (Table 3). Abundance and species richness were positively correlated in most higher level taxa, except for Arctiina, Euchromiina and Lithosiini (Table 3). However, after Bonferroni correction, species and abundance were correlated significantly only in four of the eleven taxa, i.e. Pericopina, Ctenuchina, Phaegopterina and Lithosiini without *Agylla* (Table 3).



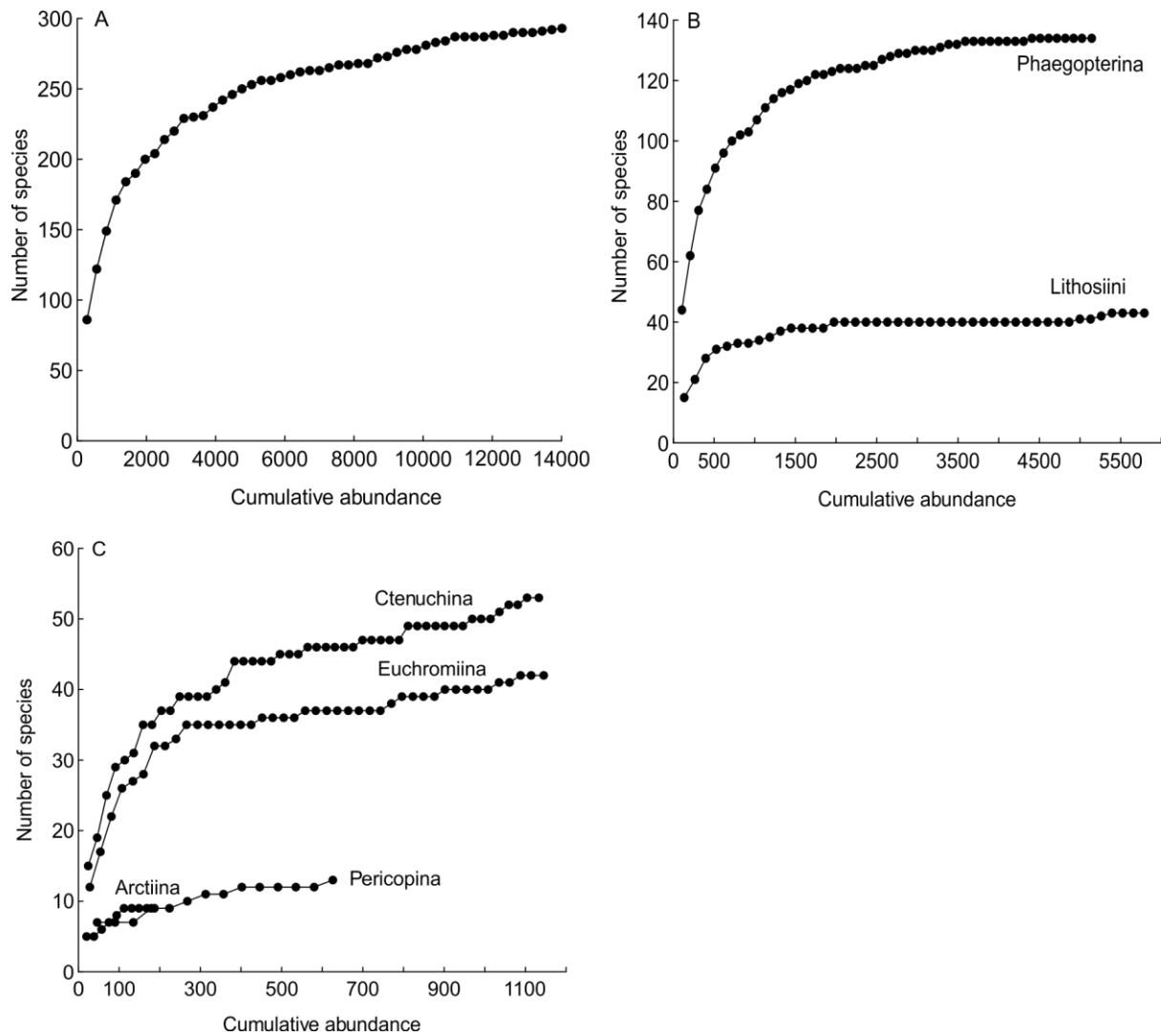
**Figure 2.** Rank abundance distribution of the total sample.

The total species accumulation curve (Fig. 3A) suggests our sample recovered the majority of species that could be sampled with automatic light traps. Lithosiini had 43 species and 5791 individuals, and accumulated species much faster than Phaegopterina, with 134 species and 5144 individuals (Figure 3B). However, when *Agylla* species were removed Lithosiini accumulated species much faster than *Agylla* (species accumulation curves not shown). Ctenuchina and Euchromiina species richness differed (53 and 42), but with similar abundances (1133 and 1145), and similar species accumulation curves (Fig. 3C). In the total sample Pericopina and Arctiina had the lowest richness (13 and 9 species) and abundance (626 and 187 specimens), and Arctiina accumulated species faster than Pericopina (Fig. 3C).

**Table 3** Spearman rank correlation between richness and abundance, and between elevation and: richness abundance and dominance for Arctiinae and its main subordinated taxa. Printed in bold are results that remain significant after sequential Bonferroni correction. Significance levels: \* < 0.05, \*\*<0.005, \*\*\*,0.001.

|                                  | Corr. between richness and abundance | Corr. between elevation and richness | Corr. between elevation and abundance | Corr. between elevation and dominance |
|----------------------------------|--------------------------------------|--------------------------------------|---------------------------------------|---------------------------------------|
| Arctiinae                        | 0.76*                                | 0.31                                 | 0.71*                                 | 0.8*                                  |
| Arctiini                         | 0.8*                                 | 0.31                                 | 0.58                                  | 0.15                                  |
| Arctiina                         | 0.04                                 | 0.27                                 | -0.2                                  | -0.51                                 |
| Pericopina                       | <b>0.83*</b>                         | 0.54                                 | 0.78*                                 | -0.65                                 |
| Ctenuchina                       | <b>0.86**</b>                        | -0.008                               | 0.25                                  | 0.08                                  |
| Euchromiina                      | 0.56                                 | 0.11                                 | 0.68                                  | 0.21                                  |
| Ctenuchina+Euchromiina           | 0.73*                                | 0.05                                 | 0.56                                  | 0.01                                  |
| Phaegopterina                    | <b>0.88**</b>                        | 0.52                                 | 0.51                                  | 0.36                                  |
| Lithosiini                       | 0.15                                 | -0.06                                | 0.81*                                 | <b>0.8*</b>                           |
| Lithosiini without <i>Agylla</i> | <b>0.907***</b>                      | -0.49                                | -0.5                                  | 0.016                                 |
| <i>Agylla</i>                    | 0.79*                                | <b>0.91***</b>                       | 0.85*                                 | 0.55                                  |

There was no correlation between elevation and species richness for higher level taxa (Table 3), but there was a strong positive correlation for *Agylla* alone ( $p = 0.91$ ,  $P < 0.001$ ). Abundance correlated positively with elevation in Arctiinae, and also Pericopina and Lithosiini. However, when *Agylla* was removed from Lithosiini this correlation was lost. Not surprisingly, a positive correlation between elevation and abundance was found for *Agylla* alone. Despite these results there was no significant correlation between abundance and elevation in any analyzed taxa after Bonferroni correction (Table 3). Elevation did not correlate with number of singletons ( $n = 33$ ) nor with the proportion of singletons of each taxa (data not shown, all  $P > 0.05$ ). Species richness and abundance for nine sampling sites with 20-24 sampling nights are shown in Table 4.



**Figure 3.** Species accumulation curves: A) Total sample. B) Phaegopterina and Lithosiini. C) Ctenuchina, Euchromiina, Pericopina and Arctiina.

### 3.2 Community similarity

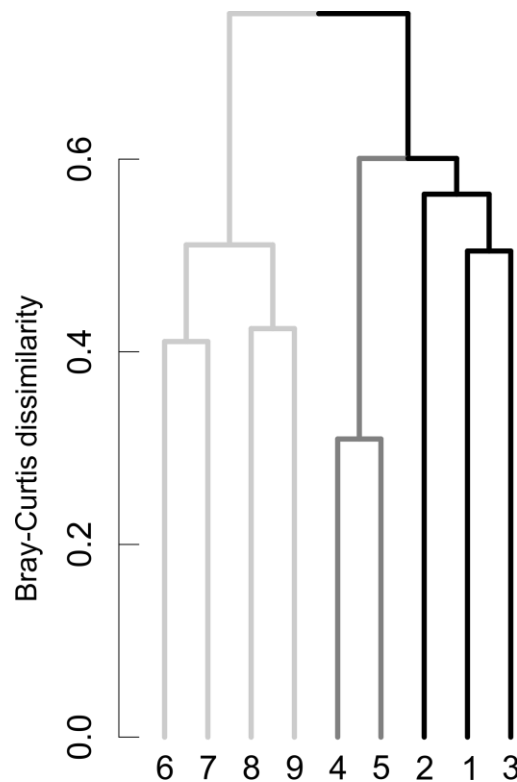
Cluster analysis based on Bray-Curtis index indicated that arctiine community similarity in the study area followed a vegetation structure gradient from lowland (sites 1-3) to submontane (sites 4 and 5), and montane forest (sites 6-9) (Fig. 4). Furthermore, the clustering pattern indicates that the submontane arctiine fauna (4-5) is more similar to that found in lowland (1-3) rather than montane sites (6-9).

**Table 4.** Species richness (S) and abundance (N) of selected Arctiinae subordinated taxa from site number 1 to 9.

|                           |   | 1   | 2   | 3   | 4   | 5   | 6    | 7    | 8   | 9    | Total |
|---------------------------|---|-----|-----|-----|-----|-----|------|------|-----|------|-------|
| Arctiini                  | S | 92  | 78  | 125 | 123 | 117 | 166  | 133  | 97  | 109  | 245   |
|                           | N | 325 | 443 | 521 | 813 | 998 | 1998 | 1182 | 689 | 740  | 7709  |
| Arctiina                  | S | 2   | 2   | 2   | 1   | 2   | 2    | 3    | 1   | 7    | 8     |
|                           | N | 16  | 10  | 17  | 31  | 35  | 10   | 5    | 4   | 23   | 151   |
| Pericopina                | S | 5   | 2   | 6   | 7   | 4   | 8    | 8    | 7   | 6    | 12    |
|                           | N | 23  | 6   | 20  | 34  | 32  | 176  | 140  | 35  | 109  | 575   |
| Ctenuchina                | S | 19  | 18  | 27  | 32  | 28  | 41   | 26   | 14  | 18   | 53    |
|                           | N | 56  | 44  | 76  | 108 | 106 | 450  | 132  | 50  | 65   | 1087  |
| Euchromiina               | S | 13  | 7   | 30  | 17  | 17  | 27   | 16   | 15  | 15   | 40    |
|                           | N | 27  | 14  | 95  | 42  | 38  | 484  | 193  | 54  | 157  | 1104  |
| Ctenuchina+Euchromiina    | S | 32  | 25  | 57  | 49  | 45  | 68   | 42   | 29  | 33   | 93    |
|                           | N | 83  | 58  | 171 | 150 | 144 | 934  | 325  | 104 | 222  | 2203  |
| Phaegopterina             | S | 53  | 49  | 60  | 66  | 66  | 88   | 80   | 60  | 63   | 132   |
|                           | N | 203 | 369 | 313 | 598 | 787 | 878  | 712  | 546 | 386  | 4792  |
| Lithosiini                | S | 17  | 20  | 28  | 26  | 25  | 25   | 24   | 18  | 20   | 43    |
|                           | N | 109 | 58  | 341 | 524 | 318 | 1379 | 986  | 616 | 1313 | 5644  |
| Lithosiini without Agylla | S | 7   | 12  | 18  | 14  | 13  | 13   | 10   | 3   | 5    | 25    |
|                           | N | 26  | 29  | 85  | 41  | 57  | 71   | 22   | 3   | 10   | 344   |
| Agylla                    | S | 10  | 8   | 10  | 12  | 12  | 12   | 14   | 15  | 15   | 18    |
|                           | N | 83  | 29  | 256 | 483 | 261 | 1308 | 964  | 613 | 1303 | 5300  |

### 3.3 Proportion of taxa along sampling sites

Proportions of species richness and abundance of tribes and subtribes at sampling sites with 20-24 sampling nights are given in Fig. 5. Proportion of species richness and elevation did not correlate in any analyzed taxa, except when Lithosiini was analyzed without *Agylla*, although it was not significant after Bonferroni correction (Table 5). Elevation and abundance were negatively correlated in the subtribes Arctiina, Ctenuchina and Phaegopterina, but not in Pericopina, Euchromiina and Ctenuchina+Euchromiina, but none of these taxa correlated with elevation after P corrections (Table 5). However, when P values were adjusted, Lithosiini abundance and elevation were significantly positively correlated (Fig. 5). In contrast, when Lithosiini was analyzed without *Agylla*, elevation and abundance were negatively correlated (Table 5), but a strong positive correlation was found for *Agylla* alone.



**Figure 4.** Cluster analysis based on Bray-Curtis dissimilarity. Sites 1-3 Lowland Atlantic Forest (black lines), 4 and 5 Submontane Atlantic Forest (dark gray lines), 6-9 Montane Atlantic Forest (light gray lines). See Table 1 for altitudes.

### 3.4 Diversity measures

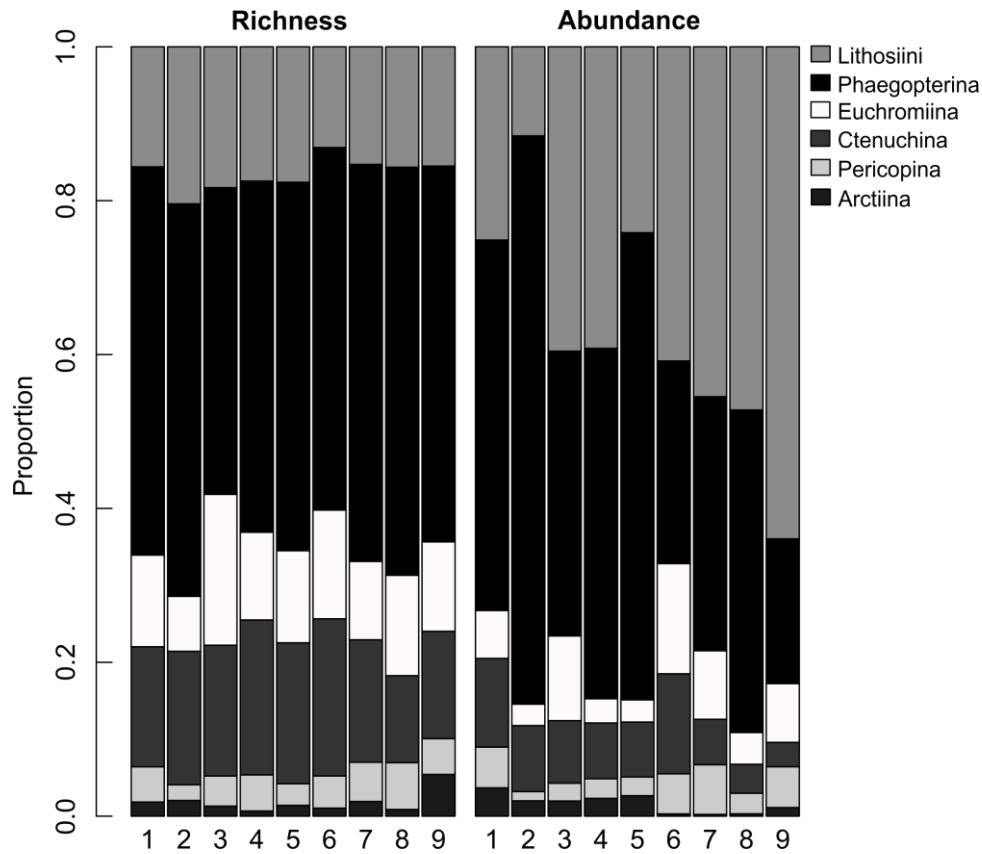
Less than 100 individuals of Arctiina and Pericopina were sampled at most sampling sites and therefore Fisher's alpha values were not calculated for these taxa. Because Ctenuchina and Euchromiina together had more than 100 individuals at all sampling sites except sites 1 and 2 (Table 4), as done in previous studies on Arctiinae diversity (Süssenbach, 2003; Hilt, 2005), Fisher's alpha was calculated for Ctenuchina+Euchromiina. We found significant deviations from the log series distribution in only three of the 54 data: site 9, Arctiinae ( $\chi^2=23.07$ ,  $p<0,05$ ), Ctenuchina+Euchromiina ( $\chi^2=12.43$ ,  $p<0,05$ ); and site 7, Lithosiini ( $\chi^2=10,16$ ,  $p<0,05$ ). Although we sampled less than 100 individuals of Lithosiini at site 2 and less than 100 individuals of *Agylla* in sites 1 and 2 (Table 4), Fisher's alpha fitted well for these data.

**Table 5.** Spearman rank correlation between elevation and proportional species richness and abundance of Arctiinae main subordinated taxa. Printed in bold are results that remain significant after sequential Bonferroni correction. Significance levels: \* < 0.05, \*\*<0.005, 0.001\*\*\*.

|                                  | Elevation and proportion of species | Elevation and proportion of specimens |
|----------------------------------|-------------------------------------|---------------------------------------|
| Arctiina                         | 0.03                                | -0.7*                                 |
| Pericopina                       | 0.58                                | 0.53                                  |
| Ctenuchina                       | -0.33                               | -0.75*                                |
| Euchromiina                      | 0.08                                | 0.28                                  |
| Ctenuchina+Euchromiina           | -0.33                               | -0.36                                 |
| Phaegopterina                    | 0.28                                | -0.7*                                 |
| Lithosiini                       | -0.55                               | <b>0.85**</b>                         |
| Lithosiini without <i>Agylla</i> | -0.78*                              | <b>-0.91**</b>                        |
| <i>Agylla</i>                    | 0.43                                | <b>0.93***</b>                        |

Values of Fisher's alpha and 95% confidence interval plotted against elevation for Arctiinae and lower categories are shown in Fig. 6. Lithosiini was the only group where values of Fisher's alpha were significantly negatively correlated with both elevation and abundance, although not after P corrections (Table 6). Values of Fisher's alpha could not be computed when *Agylla* was removed from the sample due to low abundance. For *Agylla* alone, Fisher's alpha was not correlated with elevation or abundance (Table 6). While Phaegopterina, Arctiini and *Agylla* did not show any relationship with elevation, diversity seems to decline almost linearly with increasing elevation from site 3 to 9 in Ctenuchina+Euchromiina, with initial low values for lowland sites 1 and 2 (Figure 6).

Rarefied species richness of the higher level categories in the nine sampling sites with 20-24 sampling nights are given in Figure 7, and correlation between rarefied species richness and elevation, and rarefied species richness and abundance in Table 6. Elevation and rarefied species richness were correlated in Arctiinae, Ctenuchina+Euchromiina, Lithosiini and *Agylla*, but not after P corrections. Abundance and rarefied species richness were correlated in *Agylla* and Lithosiini, but this correlation was significant only in *Agylla* after P correction. There was no correlation between rarefied species richness and abundance when Lithosiini was analyzed without *Agylla* (rarefied species richness not shown in Fig. 7).



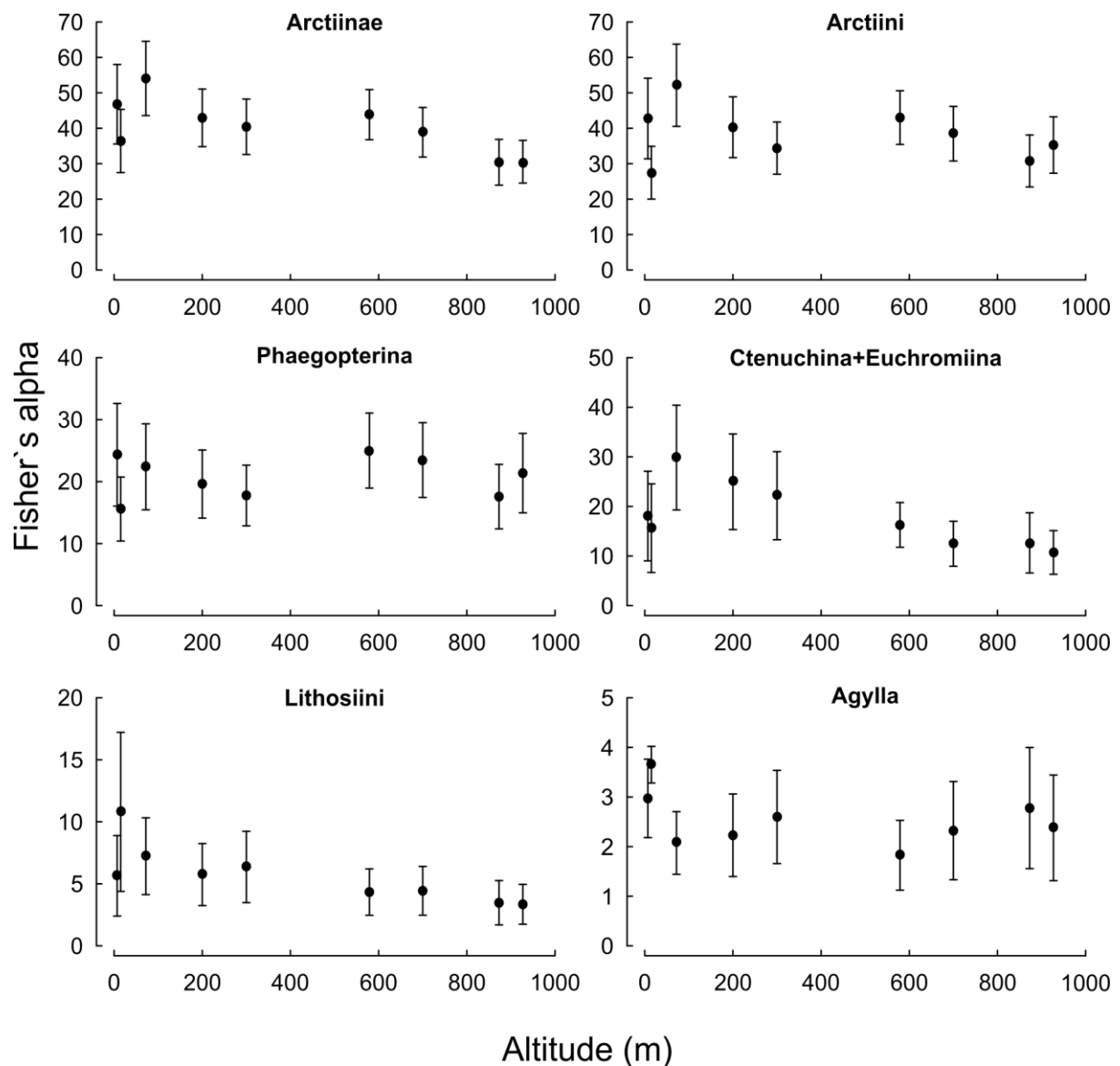
**Figure 5.** Proportional species richness and abundance of Arctiini subtribes and Lithosiini along the nine sampling sites with 20-24 sampling nights. See Table 1 for altitudes.

**Table 6** Spearman rank correlation between two diversity measures (Fisher's alpha of the log series and rarefied species number) and elevation and abundance. Rarefied species number levels: Arctiinae (400), Arctiini (300), Ctenuchina (40), Euchromiina (10), Ctenuchina+Euchromiina (50), Phaegopterina (200), Lithosiini (50), Lithosiini without *Agylla* (3), *Agylla* (29). Printed in bold are results that remain significant after sequential Bonferroni correction. Significance levels: \* < 0.05, \*\*<0.01.

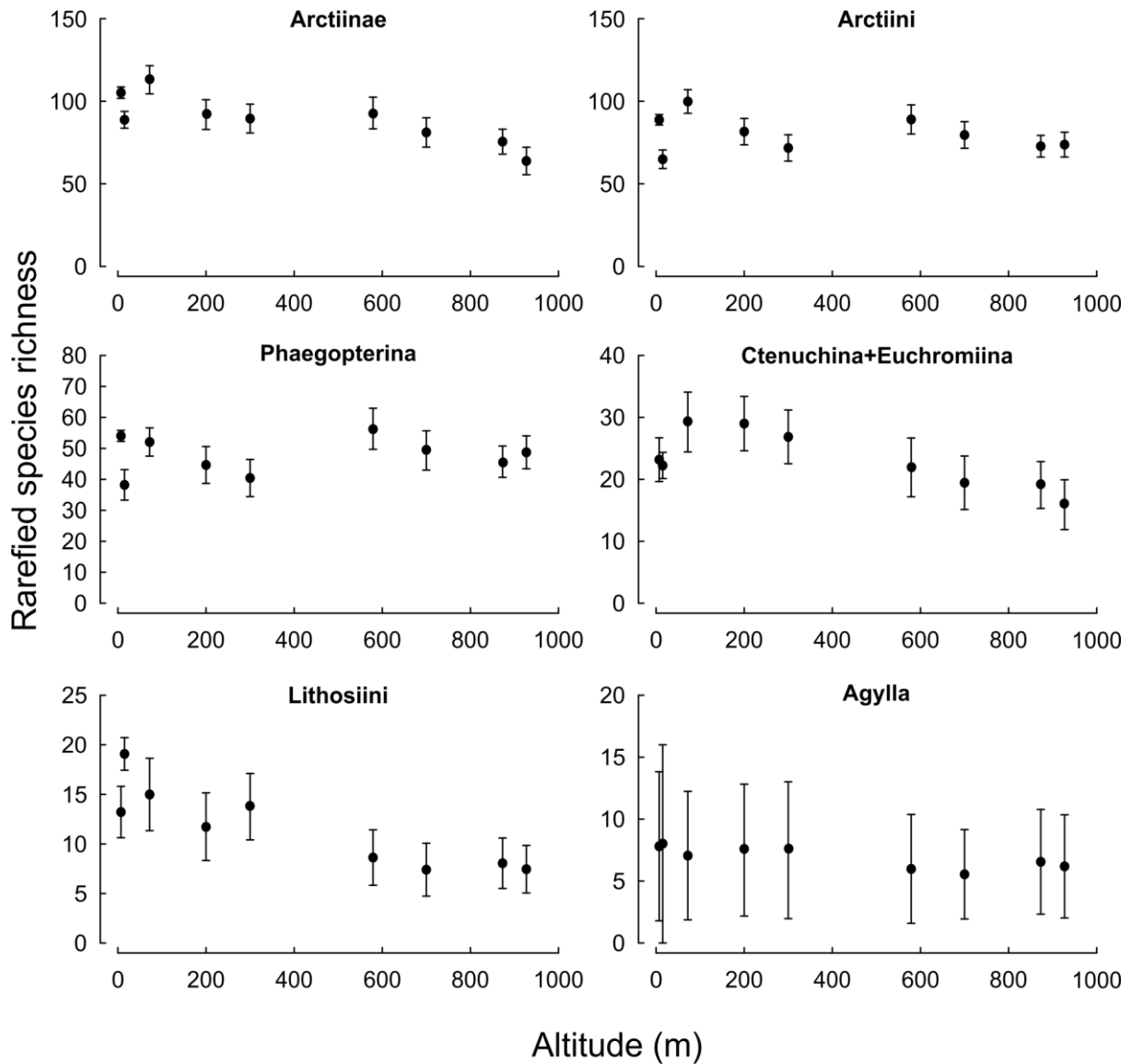
|                                  | Fisher's alpha<br>and elevation | Fisher's alpha<br>and abundance | Rarefied species<br>number and<br>elevation | Rarefied species<br>number and<br>abundance |
|----------------------------------|---------------------------------|---------------------------------|---|---|
| Arctiinae                        | -0.65                           | -0.16                           | -0.75*                                      | -0.31                                       |
| Arctiini                         | -0.25                           | 0.13                            | -0.2  | 0.08  |
| Ctenuchina                       | -                               | 0.33ns                          | -0.36                                       | 0.61  |
| Euchromiina                      | -                               | -0.33                           | -0.56                                       | -0.63                                       |
| Ctenuchina+Euchromiina           | -0.66                           | -0.16                           | -0.75*                                      | -0.21                                       |
| Phaegopterina                    | -0.03                           | 0.1                             | 0.01  | -0.05                                       |
| Lithosiini                       | -0.8*                           | -0.8*                           | -0.81*                                      | -0.81*                                      |
| Lithosiini without <i>Agylla</i> | -                               | -                               | -0.01                                       | -0.01                                       |
| <i>Agylla</i>                    | -0.26                           | -0.6                            | -0.8*                                       | <b>-0.88**</b>                              |



Figure 8 shows a rarefaction curve based upon 10,000 re-samples of the site 6 data (579 m), and its 95% confidence interval. Rarefied species richness were significantly higher in sites 1 and 3 ( $P<0.05$ ) when compared to the remaining sites. Montane sites 7-9 had a significantly lower species richness than submontane and lowland sites ( $P<0.05$ ). Species richness in site 2 was not significantly different from sites numbers 4-6.



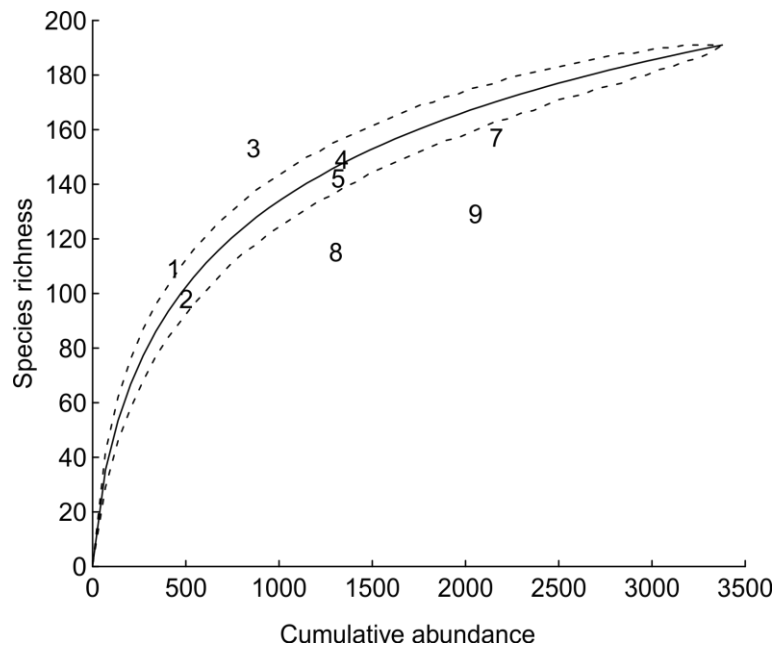
**Figure 6.** Values of Fisher's alpha of the log series for Arctiinae and its main subordinated taxa for each of the nine sites with 20-24 sampling nights. Error bars are 95% confidence intervals.



**Figure 7.** Rarefied species richness for Arctiinae and its main subordinated taxa for each of the nine sites with 20-24 sampling nights. Error bars are 95% confidence intervals. Rarefied species richness levels: Arctiinae (400), Arctiini (300), Ctenuchina (40), Euclromiina (10), Ctenuchina+ Euclromiina (50), Phaegopterina (200), Lithosiini (50), Lithosiini without *Agylla* (3), *Agylla* (29).

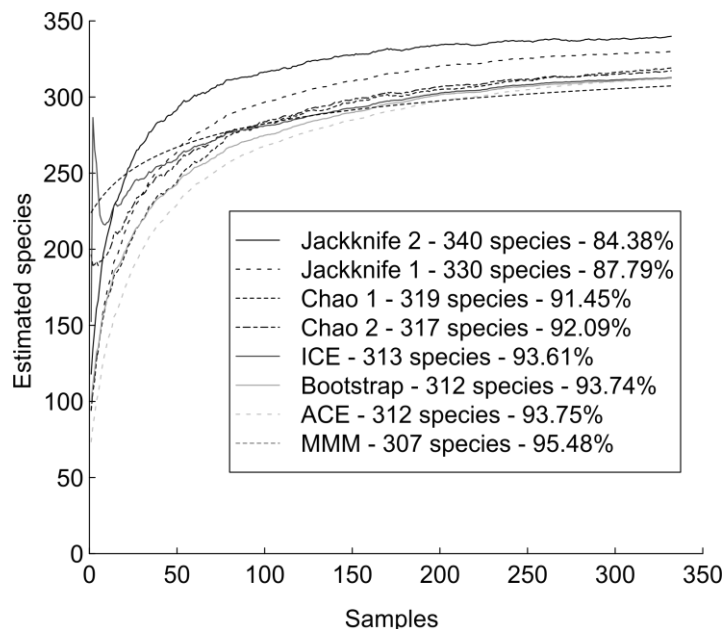
### 3.5 Estimated species richness

Figure 9 shows species richness estimation curves for the total data set resulted from nine commonly used estimators. Estimation indicated that our sampling recovered between 84.38% and 95.48% of the species richness that could be sampled in the study area with automatic light traps (see legend inserted in Fig. 9). The number of additional species found by each estimator were: MM model estimator (13); ACE and Bootstrap (19); Chao 1 (25 );



**Figure 8.** Rarefaction curve based upon 10,000 re-samples of the data for site 6 and its 95% confidence limits. Numbers indicate other sites with 20-24 sampling nights. See Table 1 for altitudes.

Chao 2 (23); Jackknife 1 (46); and Jackknife 2 (36). According to Brose & Martinez (2004), ICE and MM constitute the most reliable species richness estimators when the sample includes between 86% and 96% of the total community diversity. If that is the case, arctiine species richness in our study area is expected to fall within a range of 307 to 312 species.



**Figure 9.** Graphical representation for eight different species richness estimators: Jackknife 1, Jackknife 2, Chao 1, Chao 2, Abundance Coverage Estimator (ACE), Incidence Coverage Estimator (ICE), Bootstrap, and Michaelis Menten Model (MMM). See table inserted in the figure for estimated species numbers and percentage of sampling.

## 4. Discussion

### 4.1 Limitations and benefits of our sampling design

Our sampling effort and design appears equivalent or superior to those employed in other moth diversity studies. For instance, Brehm (2002) and Süssenbach (2003) build large data sets used in subsequent studies on alpha and beta diversity of different moth families in the Andean montane rainforest in southern Ecuador (Brehm & Fiedler, 2003; Brehm *et al.*, 2003a, b; Fiedler *et al.*, 2008). These authors used two replicates for 11 different altitudinal zones and obtained between four and eight samples for each zone. Although it is known that their sampling technique (manual collecting) can result in a higher richness (see below), these studies sampled a considerably smaller number of specimens as compared to our work. Therefore, we do not believe that the lack of spatial replicates is a serious deficiency of our sampling design. Quite the contrary, our study involved a considerably large sampling effort along time (two years) in the same sampling sites, varying from 20 to 24 samples (Table 2). Furthermore, arctiines are known to fly long distances in a single night (Yamanaka *et al.*, 2001), and our extended sampling period increased the chance to catch most species occurring in the focal altitudinal zone.

The use of automatic traps standardizes sampling, allowing for a sound statistical comparison between sites within a given study, and also future comparisons to other data sets. The obvious advantages of this method include the possibility to run traps simultaneously in different locations and with limited manpower, and the elimination of collector bias. The effectiveness of manual collecting and automatic traps for sampling nocturnal moths was evaluated in Mount Kilimanjaro, Tanzania, using geometrid moths (Axmacher & Fiedler, 2004) and in Costa Rica, using geometrids and arctiines (Brehm & Axmacher, 2006). These authors found that richness and abundance varied significantly in geometrids but not in arctiines, although species composition vary slightly between both methods in the arctiines. Despite the fact that their results are reassuring for arctiines, both were performed by the same group of researchers, and it is not guaranteed that other collectors would repeat the same performance.

The type of killing agent used in the automatic light traps affects the physical integrity of the moths, and consequently influences species identification success. We could not find any published work that evaluated the damage to specimens collected with automatic traps using different kinds of killing agents. Considering our own experience, when alcohol is used (usually 70 or 90%) the moths die fast and DNA is well preserved (see also Szinwelski *et al.*,

2012). However, a considerable amount of scales may be lost, especially when too many moths are captured in a given night. Large moths in the Saturnidae or Sphingidae are usually damaged (Mauricio M. Zenker pers. com.). Fortunately, arctiines are medium to small size and can be easily distinguished as morphospecies when compared to other Erebidae taxa (see examples of specimens collected in the abstract). It worth to note that many moths, including some arctiines, are diurnal and/or are not attracted to light (Scoble, 1995). Despite the fact that we sampled 11 specimens of the diurnally active *Pseudosphex rubripalpus* (Appendix 2I, Hogue, 1993), it is likely that diurnally active Arctiinae moths are not well represented in our sampling, and that we underestimated species richness for Serra da Graciosa.

#### 4.2 Sample size dependence

The main drawback of using species richness as a diversity measure for hyper-diverse Arthropods groups is that many specimens (i.e. a large sampling effort) is required to produce a fairly accurate diversity estimate (Colwell & Coddington, 1994). Surprisingly, the Spearman rank correlation between species richness and abundance was not significant for three taxa (Table 3), suggesting that the sample size is not adequate to produce a reliable diversity estimate in these taxa. However, abundance also varied markedly between sampling sites in the taxa where a significant correlation was not found; for instance, 95 individuals in 30 euchromiine species were collected in site 3, while 484 individuals of 27 euchromiine species were obtained in site 6 (Table 4). These discrepancies can be attributed to the presence of highly dominant species at some sites, and a high number of rare species at other sites (see Appendix 2I for details). The same applies to the weak correlation between Fisher's alpha and abundance in Lithosiini, and the weak and strong correlations between rarefied species richness and abundance in Lithosiini and *Agylla* (Table 6).

#### 4.3 Does Arctiinae alpha diversity vary with elevation?

Except for the genus *Agylla* (Table 3) we found no significant correlation between species richness and elevation in Arctiinae or subordinate taxa, but we did find a weak correlation between elevation and abundance and elevation and dominance (Table 3). It was evident that these correlations were strongly influenced by Lithosiini (Table 3), in addition to the correlations between abundance proportion and elevation (Table 5). Most Lithosiini species were small (20-30mm wingspan), but species of *Agylla* were large (about 35-60 mm wingspan). The abundance of these two size categories were both correlated with elevation, but in a reciprocal manner: elevation and abundance was negatively correlated for Lithosiini

without *Agylla*, but positive for *Agylla* alone (Table 5). There was also a positive correlation between species richness and elevation for *Agylla*, and a slight negative correlation in Lithosiini without *Agylla* (Table 3).

Except for a weak correlation in Lithosiini, Fisher's alpha was not correlated with elevation in Arctiinae or subordinate taxa (Table 6). However, rarefied species richness and elevation did correlate for the subfamily as a whole, and Ctenuchina+Euclorini, Lithosiini and *Agylla* (Table 6; Fig 7). Thus, there was no consistent relationship between diversity and elevation in Arctiinae, excepting for Lithosiini. However, it is worth to note that rarefaction analysis based on site six (mid elevation) showed that diversity is lower at higher elevation sites.

The association between elevation and environmental variables such as temperature, relative humidity, and rainfall is well known. Although these variables were not directly measured at the sampling sites during this study, temperature decrease was estimated as 0.54 to 0.56 °C every 100 m upwards, with relative humidity and rain fall considerably lower at the upper part of the elevational gradient (Roderjan, 1994; Rocha, 1999). Thus, the results for the elevational gradient at Serra da Graciosa may reflect a temperature and relative humidity and rainfall gradients. It is especially true for community composition since Cluster analysis based on Bray-Curtis index showed that species similarity changes according to the vegetation structure gradient (Fig. 4), which is also determined by the elevation.

It worth to note that abundance was markedly reduced in site FE (Fig. 1A, Table 2, Appendix 2I), possibly due to livestock impact on the herbaceous vegetation (see also Hilt & Fiedler, 2005). For conservation purposes, large blocks of natural montane forests must be preserved, and grazing animals must be excluded from such areas.

#### 4.5 Arctiinae diversity in a broad geographical scale context

Arctiinae diversity in tropical mountains of Central and South America appear to be higher than in other areas of the world (see Brehm, 2009 for a list of studies). Diversity is astonishingly high in the Andean montane rainforest of Southern Ecuador, where Süssenbach (2003) sampled 4,491 specimens of 415 species, and our study sampled 14,026 specimens of 294 species, although different sampling approaches were used. Values of Fisher's alpha for Arctiinae ranged from 24 to 59 in Southern Ecuador, and ranged from 30.4 to 54.06 at our sites. Süssenbach (2003) found no significant correlation between elevation and diversity in Arctiinae, but rather a significant negative correlation for Lithosiini only, and that *Agylla* was the most abundant genus containing many individuals that could not be identified to the

species. These results were similar to ours, especially considering that the studies were located in different altitudinal zones, and in mountain ridges that are physiognomically and biogeographically different.

**Table 7** Comparisons between five different works accessing Arctiini diversity in three different Brazilian biomes using automatic light traps. AF – Atlantic Forest, P – Pampa, OA – Oriental Amazon (See Appendix 3I for sampling sites locations).

\*Total data set for Arctiini only. \*\*Data set for site number 4 considering Arctiini only. \*\*\*Data considering the sampling site at 235m a.s.l. only. S: species richness; N: abundance.

| Study                       | Biome | Elev (m) | Samples | Sampling sites | S   | N    | Fisher's alpha | Singletons |
|-----------------------------|-------|----------|---------|----------------|-----|------|----------------|------------|
| This study*                 | AF    | 9-927    | 224     | 14             | 251 | 8235 | 48.9           | 33         |
| Teston & Corseuil (2004)    | AF, P | 7-830    | 258     | 12             | 192 | 9800 | 33.85          | 32         |
| Teston et al. (2006)        | AF, P | 11-700   | 40      | 40             | 137 | 5924 | 24.82          | 19         |
| This study**                | AF    | 200      | 23      | 1              | 123 | 813  | 42.93          | 48         |
| Teston & Corseuil (2004)*** | AF    | 235      | 48      | 2              | 114 | 2632 | 24.28          | 19         |
| Teston & Delfina (2010)     | OA    | 130      | 24      | 1              | 64  | 420  | 21.03          | 26         |
| Teston et al. (2012)        | OA    | 195      | 24      | 1              | 78  | 466  | 26.78          | 44         |

Recent surveys on tiger moth diversity in the southern limits of Brazilian Atlantic Forest, Pampa and Oriental Brazilian Amazon have produced species lists and abundance patterns (see sampling sites and references in Appendix 3I). Teston and Corseuil (2004) investigated Arctiini diversity in six southern Brazilian regions between 7 and 830 m a.s.l., three in the Atlantic Forest and three in the Pampa. Using traps almost identical to ours and a comparable sampling effort, these authors found a considerably lower species richness (Table 7). In a rapid biodiversity assessment in four state parks also located in these biomes, Teston *et al.* (2006) found lower species richness than our study. In both cases Fisher's alpha corroborated the lower diversity of their sites in relation to our study area (Table 7). It is known that moth diversity is considerably lower in the Pampa than in the Atlantic Forest (Specht, 2001; Teston & Corseuil, 2004; Ferro & Teston, 2009). This pattern can be attributed to the predominance of grasses in the Pampa, while plant diversity is much higher in the Atlantic Forest (Ferro & Melo, 2011).

**Table 8** Comparisons between diversity of Arctiini in three elevational zones in different locations in the Atlantic Forest using automatic light traps. See figure 1 and 2 for sampling site locations of this study, and Appendix 3I for sampling site locations of Teston & Corseuil (2004).

| Study                    | Elev. (m) | Samples | Sampling sites | S   | N    | Fisher's alpha | Singletons |
|--------------------------|-----------|---------|----------------|-----|------|----------------|------------|
| Teston & Corseuil (2004) | 235       | 48      | 2              | 114 | 2632 | 24.28          | 19         |
| This study               | 200       | 23      | 1              | 123 | 813  | 42.93          | 48         |
| Teston & Corseuil (2004) | 556       | 44      | 2              | 105 | 2554 | 22.05          | 27         |
| This study               | 579       | 23      | 1              | 166 | 1998 | 43.83          | 46         |
| Teston & Corseuil (2004) | 830       | 40      | 2              | 72  | 666  | 20.5           | 28         |
| This study               | 873       | 23      | 1              | 97  | 689  | 30.4           | 38         |

A consolidated pattern emerged when diversity of arctiins in the southern limits of Brazilian Atlantic Forest, Pampa and Oriental Brazilian Amazon was carefully evaluated, although one single cause may not explain this pattern. Diversity was also lower in the Oriental Brazilian Amazon in relation to Serra da Graciosa (Table 7), and when we compared sampling sites within the same altitudinal range between Serra da Graciosa and those in Teston and Corseuil (2004) (Table 8) it was clear that Serra da Graciosa was much more diverse. There are two possible explanations for this finding. (1) Our sampling sites were located along an elevational transect and were close to each other, and thus there could be a flow of specimens between them. In contrast, sites sampled by Teston and Corseuil (2004) were distantly located from each other and with no flow of specimens between them. (2) It is also known that plant community affects Arctiinae diversity, as demonstrated by Ferro *et al.* (2010) in the Brazilian Cerrado. These authors observed markedly longitudinal similarity distance decay in a broad geographical scale area in central Brazil, and hypothesize that this pattern is related to host-plant availability. It is worth to note that the insect/host-plant relationship in Arctiinae may be very complex: species referred to as “polyphagous” can require pyrrolizidine alkaloids from one host but feed on several other nontoxic host-plants, changing host-plant back when pyrrolizidine alkaloids are required again (Singer & Bernays, 2009). In addition, many arctiines species, especially lithosins, feeds on lichens and mosses (Scoble, 1995), with little or no available information about its hosts in the Neotropics.

## 5. Conclusions

The recorded species richness and diversity of the tribe Arctiini in the Serra da Graciosa is the highest ever measured in Brazil. Although there is no agreement between Fisher's alpha of the log series and rarefied species richness, rarefaction analysis suggests



that diversity is higher near the sea level instead of mid elevations. However, as the elevational range sampled (7-927m) do not represent the entire local elevational gradient (0-1500m) we were not able to attest whether diversity is lower in higher elevation, therefore future studies are needed to test this hypothesis. The positive correlation between abundance and elevation, and dominance and elevation in Arctiinae was attributed exclusively to the Lithosiini, especially to the highly abundant *Agylla* species. The abundance of the smallest Lithosiini species correlated negatively with elevation and the abundance of largest species, represented by the genus *Agylla*, correlated positively. This study represents the first great effort to understand diversity of Tiger moths along elevational gradients in Brazil. Therefore, it is expected that further studies on evolution, host plant distribution and natural history clarify the patterns we found.

#### Acknowledgements

We would like to thank the Brazilian government funding agencies CNPq (Conselho Nacional de Desenvolvimento Científico e Tecnológico, process number 141142/2009-0) and CAPES (Comissão de Aperfeiçoamento de Pessoal de Nível Superior, process number 5708-11-7) for the first author's scholarships. We gratefully acknowledge the University of New Orleans (USA) for the support during the period when the first author visited this institution and to Dr. Michel Laguerre (Institut Européen de Chimie et Biologie, France) for the identification of the Lithosiini species, and Dr. Viviane G. Ferro for the collaboration. Finally, we especially thank all the inhabitants of the Serra da Graciosa for the great help during the course of this study.

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## Chapter 2: Seasonal and altitudinal diversity patterns of Tiger moths in the Atlantic forest, Brazil

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**Abstract:** Understanding seasonal and altitudinal patterns of biodiversity are essential to plan and implement conservation actions in threatened habitats. We sampled a community of the moth subfamily Arctiinae during two consecutive years in the Atlantic Forest of southern Brazil to assess altitudinal and seasonal diversity patterns from Lowland to Montane forest (~1000m a.s.l). Abundance and species richness tend to increase from sea level (Lowland) to mid-elevation (Montane) with Montane being significantly more abundant than Lowland and Submontane, but rarefaction analysis indicated that diversity is higher in Lowland, while Fisher's alpha of the log series showed no difference between Lowland and Montane. Abundance was marginally significant different among seasons in the three elevations, but increased significantly in Montane during the wet season when compared to Submontane and Lowland. Rarefaction analysis showed that diversity was higher during the wet season in Montane and during the dry season in Lowland and Submontane. NMDS analysis indicated that community change gradually from Lowland to Montane, and ANOSIM analysis showed no difference between Lowland and Submontane during the dry season. Community composition in the southern limits of the Atlantic Forest is different from our sampling site, and the ordination revealed no influence of altitude since sampling sites are geographically distant.

**Key words:** Altitude, insect conservation, Mata Atlantica, Arctiidae, Abundance.

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### 1. Introduction

Diversity in space and time along various gradients has been documented in a number of arthropod groups including butterflies (e.g. Ribeiro et al. 2010, DeVries et al. 2012, Grotan et al. 2012), beetles (e.g. Jay-Robert et al. 2008, Maveety et al. 2011), ants (e.g. Albrecht & Gotelli 2001, Marques & Del-Claro 2006), spiders (e.g. Cardoso et al. 2007, Hsieh & Linsenmair 2012) and other taxa (e.g. Wolda 1992, Schulze & Fiedler 2003). Although several quantitative (e.g. Brehm et al. 2003b, Süssenbach 2003) and qualitative studies (Beck & Kitching 2009) on tropical moths diversity along elevational gradients have been done recently, few have addressed altitudinal and seasonal diversity patterns simultaneously.

Since elevational temperature gradients are more pronounced than latitudinal gradients (Colwell et al. 2008), data on altitudinal diversity patterns is essential to monitor elevational range shifts and lowland biotic attrition from climate change. The importance of knowing seasonal patterns lies in the fact that targets of conservation actions (species or higher taxonomical categories) may be active during a restricted period of time along the year. Moreover, some moth taxa are used as indicators of diversity and/or environmental quality (New 1997, Kitching et al. 2000), and a few have agricultural (Holloway et al. 1992) and medical importance (Specht et al. 2008). Therefore, information on seasonal activities patterns, allied with the record of environmental factors of temperature and rain fall, can help scientists plan and implement actions to use these insects as our allies or to fight them.

Arctiine moths, the so called Tiger Moths (adults) or Woolly Bears (larvae), are notable for their bright colors and capacity to feed on toxic host plants to acquire Pyrrolizidine Alkaloids (PA) (Weller et al. 1999, Hartmann 2009), that function as a defense against predators (e.g. Eisner & Eisner 1991). The Arctiinae is included in the highly speciose Noctuoidea as a clade of Erebidae (Zahiri et al. 2011; Zahiri et al. 2012), and is distributed worldwide with approximately 11,000 described species grouped in three major lineages (i.e. Arctiini, Lithosiini and Syntomini) (Jacobson & Weller 2002).

Arctiine diversity has been studied along a variety of gradients such as vegetation succession (Hilt 2005, Hilt & Fiedler 2005, 2006, Noske et al. 2008), vertical forest stratification (Schulze et al. 2001, Brehm 2007), and elevation (Sussenbach 2003; Fiedler et al. 2008; Beck et al. 2011) especially in the Andean montane forests of Ecuador, Costa Rica, and Borneo. The diversity of Arctiinae in Brazilian Atlantic Forest, a highly threatened biome and one of the world hotspots for conservation (Myers et al. 2000, Brummit & Lughadha 2003), was recently summarized by Ferro and Mello (2011) from museum specimens and published species lists. Although natural history museums as sources of spatial and temporal distribution of species is valuable, the information is sometimes biased because such records can show patchy spatiotemporal coverage (Graham et al. 2004). Robust insights into patterns of biodiversity, therefore, require standardized sampling efforts in space and time.

Using UV light traps we sampled a community of Arctiinae moths along an altitudinal transect in Atlantic Forest of Southern Brazil during two consecutive years to address the following questions: (1) Does the community vary in abundance, species richness and diversity along altitude and seasons? (2) Does abundance of dominant species vary along different altitudes and seasons? After exploring these questions we examine spatiotemporal  $\beta$  diversity in our altitudinal transect, and discuss our results with those of in previous work,

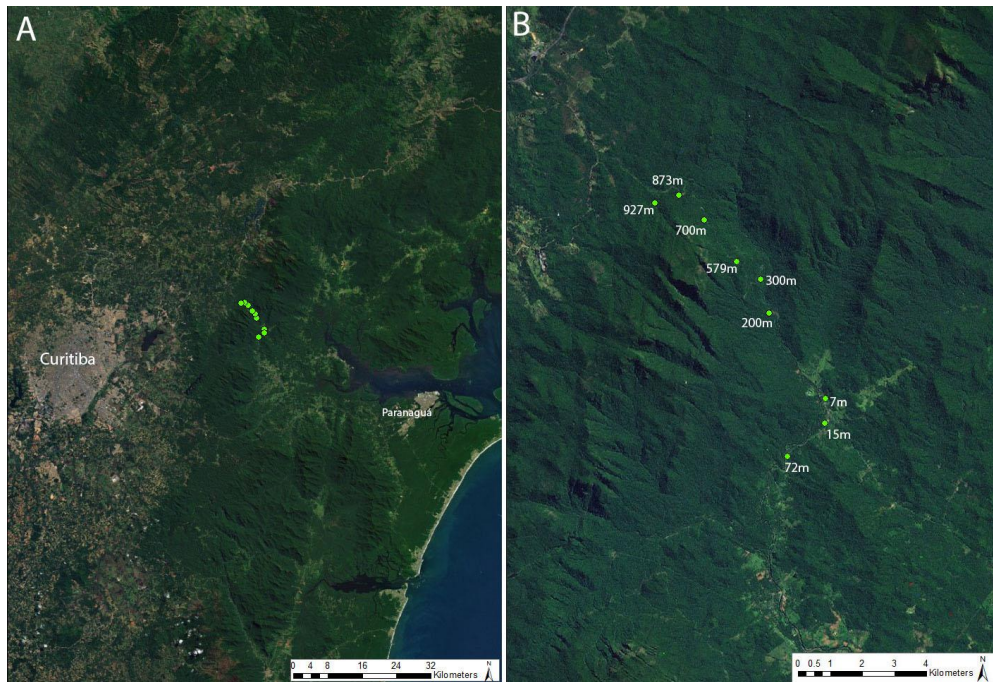
including a study from the southern limits of the Atlantic Forest with comparable sampling to the present work.

## **2. Material and methods**

### **2.1 Study area**

The study area is situated in the mountain region of Serra do Mar of southern Brazil, Paraná State. We used the State Road PR-410 (Graciosa Road) as a transect through Graciosa Ridge to assess nine sampling sites with altitude between 7 and 927m (Fig. 1). We used vegetation structure and physiognomy to establish altitudinal gradient categories, as stated elsewhere (Veloso et al. 1991, Roderjan et al. 2002). Three sites were included in Lowland Forest (7-72m), two sites in Submontane Forest (200-300m) and four sites in Montane Forest (579-927m). To represent microhabitat variation in the area, understory and at least one small clearing site was sampled in each vegetation type/elevation, except in Submontane (Table 1). Although Arctiinae diversity can vary markedly with vegetation succession (Hilt & Fiedler 2005, Hilt & Fiedler 2006), both understory and small clearing sampling sites were inside a large section of primary forest, and no clearing site was larger than 1000 m<sup>2</sup>. Sampling in these clearings was done near the forest edge, perhaps making them best characterized as forest edge. However, for descriptive purposes the term small clearing is used in Table 1.

Mean temperature in the upper and lower part of the gradient may oscillates from 13.1–20.5C° to 16.6–24.7C°, respectively (IAPAR 2012). The coldest period of the year is between April and September (autumn and winter) when temperature can fall below freezing, especially at high altitudes (Vanhoni & Mendonça 2008); teperatures are higher from October to March (spring and summer) sometimes exceeding 30 C°. The recorded rainfall is higher in the lower part of the gradient (78.7-300mm) than in the upper part (71.6-193.1mm) (IAPAR 2012). As we were unable to record environmental variables directly in our sampling sites, temperature and rainfall data recorded during the sampling period were obtained from two meteorological stations of SIMEPAR (SIMEPAR Institute of Technology, [www.simepar.com.br](http://www.simepar.com.br)) located in the upper and lower parts of the gradient (Fig. 2). Statistical comparision between sampling periods were performed considering differences between years (2010 and 2011) and combing the monthly data of autumn and winter (dry season) and spring and summer (wet season). The words “dry”and “wet” are here used to designate two periods of the year with distinct meteorological characteristics and do not represent true wet and dry seasons.



**Figure 1.** A) Study area overview, Serra do Mar mountains (Paraná State, Brazil) and nearby localities. B) Road used as a transect (PR-410 Graciosa Road) and sampling sites in Serra da Graciosa. Sampling and taxonomic assignment.

We used automatic light traps (model Pennsylvania, Frost 1957) because they allowed all traps to be run simultaneously, minimize collector bias, and maximize sampling. The traps consisted of a white cloth funnel attached to a metallic frame, and a Sylvania 20W UV fluorescent tube, model W20T12 that emitted light at 356 nm (see details at [www.sylvania.com](http://www.sylvania.com)). We attached a 2 L plastic bucket filled with 90% alcohol as killing agent to the base of the funnel (Specht & Corseuil 2002; Teston & Corseuil 2004).

One light trap was located at each sampling site, with an average distance of 1296 m from each other. Light traps were operated monthly, from February 2010 to January 2012, and simultaneously at most the sites from sunset to dawn (see Results for details on sampling). To avoid bias caused by effects of moonlight and meteorological factors (Yela & Holyoak 1997, McGeachie 1998), we restricted sampling from first quarter to third quarter moon periods, preferably during new moon, and during nights with air temperature at or higher than 10 C°. Arctiins were sorted and representative specimens (at least three, when available) of each morphospecies were pinned for visual identification of wing and body color patterns; the remaining specimens were identified by comparison to the pinned specimens, dried, and stored in envelopes. All specimens were deposited at Laboratório de Dinâmica Evolutiva e Sistemas Complexos, Universidade Federal do Paraná, Curitiba-PR,

Brazil. Tissue samples of representative specimens were sent to Canadian Centre for DNA Barcoding to obtain partial COI sequences for future studies. Images and identifications of pinned specimens can be accessed at the Barcode of Life Database, [www.boldsystems.org](http://www.boldsystems.org), under the project “Lepidoptera of Serra do Mar”.

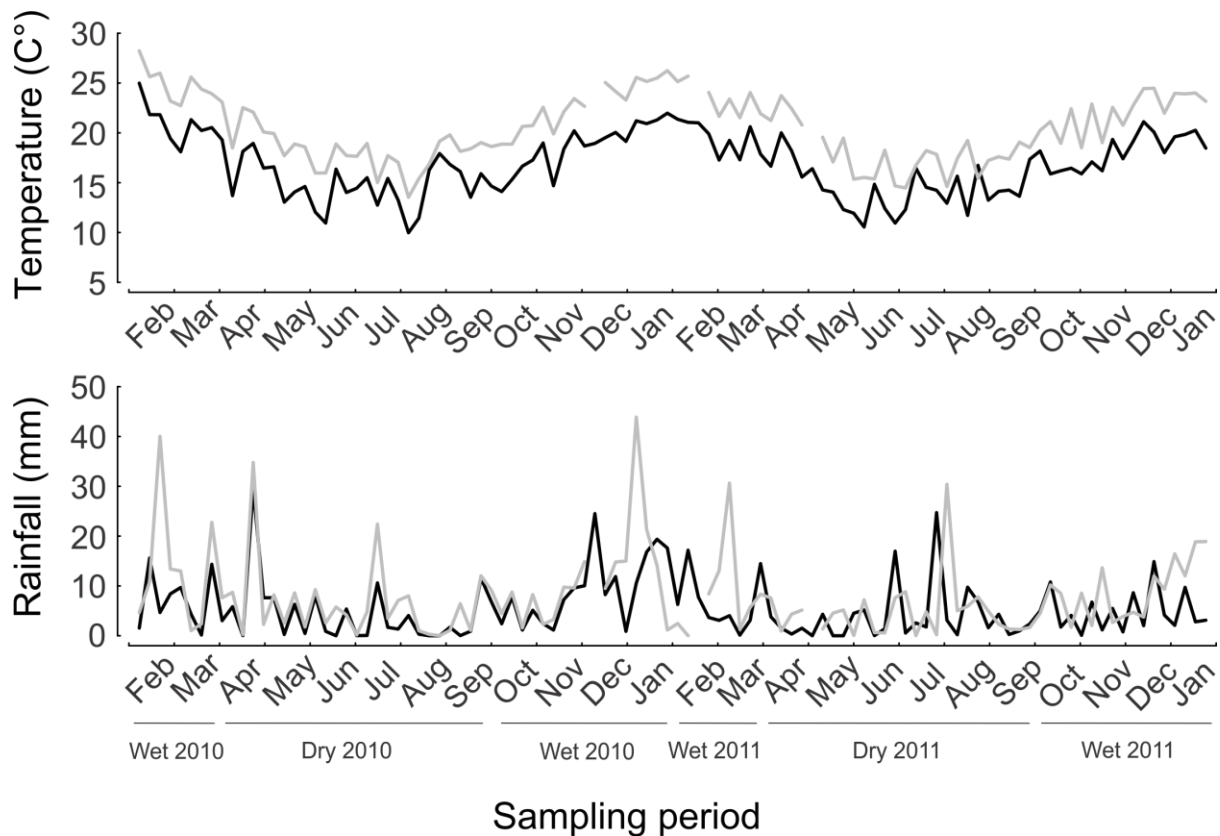
**Table 1.** Sampling sites and respectively altitudes, coordinates and details about vegetation and habitat characteristics.

| Site | Altitude | Vegetation type | Habitat characteristics | Latitude (s) | Longitude (w) |
|------|----------|-----------------|-------------------------|--------------|---------------|
| 1    | 7m       | Lowland         | Small clearing          | 25°23'6.72"  | 48°51'39.65"  |
| 2    | 15m      | Lowland         | Understory              | 25°23'29.02" | 48°51'39.89"  |
| 3    | 72m      | Lowland         | Small clearing          | 25°23'59.47" | 48°52'17.54"  |
| 4    | 200m     | Submontane      | Understory              | 25°21'49.09" | 48°52'35.89"  |
| 5    | 300m     | Submontane      | Understory              | 25°21'18.47" | 48°52'44.49"  |
| 6    | 579m     | Montane         | Small clearing          | 25°21'2.83"  | 48°53'8.96"   |
| 7    | 700m     | Montane         | Understory              | 25°20'24.51" | 48°53'40.87"  |
| 8    | 873m     | Montane         | Understory              | 25°20'2.39"  | 48°54'6.88"   |
| 9    | 927m     | Montane         | Small clearing          | 25°20'9.62"  | 48°54'31.04"  |

Species of Arctiini were identified by J.A.T. based on Brazilian collections cited in Teston and Corseuil (2002, 2003b, a). Arctiini specimens identified to genus level were assigned to five subtribes following Teston and Corseuil (2002). Where genus level identification was not possible, specimens were assigned to subtribes based on external morphology and color pattern. Lithosiini specimens were identified by Dr. Michel Laguerre based on the collections of the Natural History Museum (London) and Muséum National d'Histoire Naturelle (Paris). Subtribal classification for Lithosiini specimens was not possible due to unavailability of Neotropical species checklists Higher level classification followed Jacobson & Weller (2002), Zahiri et al. (2011), Zahiri et al. (2012).

## 2.2 Data analysis

To allow parametric statistical comparisons, we pooled the sampling sites within each altitudinal range, and monthly data sets were partitioned by wet and dry seasons. All analysis were run in R (R development Core Team 2012), unless noted otherwise.



**Figure 2.** Mean monthly temperature and rainfall (divided by week) recorded during the sampling period. Data were obtained from two meteorological stations in nearby study area. Station one (Pinhais: 893m a.s.l) was located approximately 30Km from the study area (data plotted in black line), and station two (Antonina: 20m a.s.l), approximately 15Km (data plotted in gray line). See Material and Methods for the definition of “wet” and “dry” season. The average differences of temperature and rainfall between the two stations were 3.7°C and 2.47mm, respectively. Interruptions in lines are missing data.

We used Fisher’s alpha as a measure of diversity because it is a robust and comprehensible description of community diversity and can be used even when the log series distribution is not the best descriptor of the underlying species abundance pattern (Magurran 2004). Goodness of fit tests confirming log series distribution were obtained with the program SDR4 (Henderson & Seaby 1998). We used two-way ANOVA to compare total abundance and Fisher’s alpha between years and seasons, and a two-way repeated measures ANOVA approach to compare abundance and Fisher’s alpha between altitudinal levels and seasons. Abundance data were log transformed (log10) because raw data were not well-modeled by a normal distribution, and the assumption of normality was tested using Levene test. We tested differences in abundance between altitudinal levels and seasons with individual two-way ANOVA tests for the 24 species with more than 100 specimens. In the



case of four species restricted to only one altitudinal level, we tested abundance differences between wet and dry seasons with t tests.

Rarefaction curves and rarefied species number have been widely used to compare Lepidoptera diversity along gradients such as elevation (Brehm et al. 2003a, Axmacher et al. 2004, Beck 2005), vegetation succession (Hilt & Fiedler 2005), and forest canopy and understory (DeVries et al. 1997, 2012; DeVries & Walla 1999). We used individual rarefaction curves based upon 10,000 re-samples of the total data set and its 95% confidence intervals to test whether rarefied species richness differed between elevation and sampling periods. We used the same procedure for all elevations to test for differences between years and seasons. The rarefaction curves and their 95% confidence limits were performed using EcoSim Professional Ver. 1.2d (Entsminger 2012).

Data on moth ensembles for the nine sampling sites, wet and dry seasons in 2010 and 2011, and the three elevations were ordinated using nonmetric multidimensional scaling (NMDS, with 999 permutations) based on Bray-Curtis dissimilarities to graphically show potential differences (Oksanen et al. 2008). The scores of the first NMDS axis obtained for individual sampling sites were correlated with elevation, and we repeated the same procedure with the first axis from seasonality data with temperature and rain fall. Along with the NMDS ordination, analysis of similarities (ANOSIM), also based on Bray-Curtis dissimilarities, were done to test for differences between seasonality and elevation. NMDS and ANOSIM were also used to compare our data with data on moth ensembles in the southern limit of Atlantic Forest and Pampa Biome (see discussion section).

### **3. Results**

A total of 201 sampling nights distributed along 24 consecutive months and nine sampling sites produced 13350 specimens belonging to 288 species. Number of sampling nights, species and abundance distributed among years, seasons and altitudinal levels are given in Table 2, and graphical representations of abundance and species richness in Figure 3a and 3b, respectively. Total sampling effort in 2010 was 101 nights and 100 sampling nights in 2011 (Table 2). We identified 154 taxa at species level, 96 at genus level and 39 at subtribe level. A list of species classified to tribes and subtribes with abundance data for the nine sampling sites is given in Appendix 1I.

### 3.1 Abundance, species richness and diversity

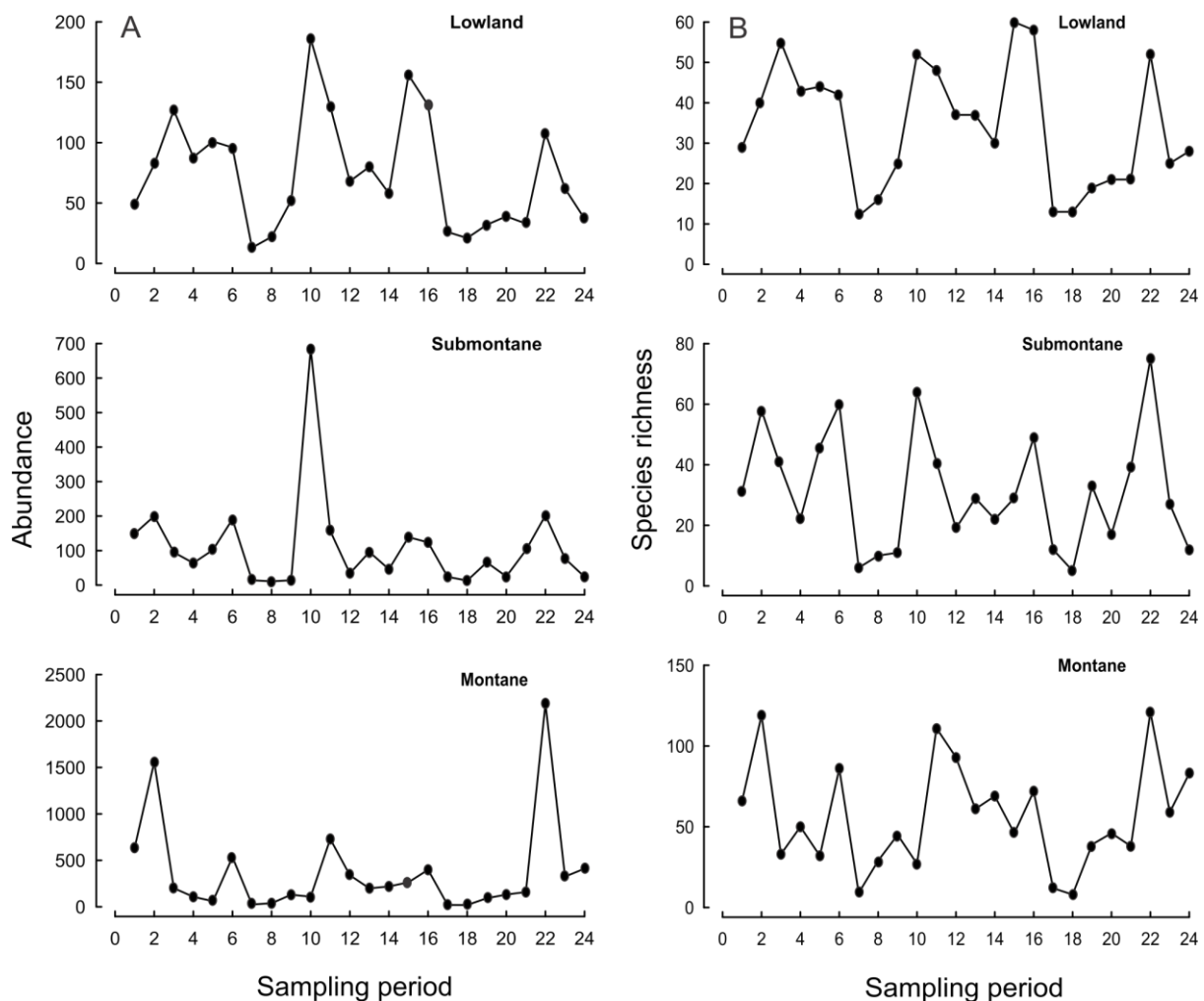
Abundance was higher in 2010 ( $N = 7201$ ) than in 2011 ( $N = 6149$ ), but not significantly so (two-way ANOVA:  $F_{1:20} = 0.29$ ,  $P > 0.05$ ). Although species richness was marginally different between years (255 in 2010, and 252 in 2011), rarefaction analysis indicated there were significantly fewer species in 2010 (Fig. 4). Fisher's alpha in 2010 (51.6) was lower than in 2011 (52.95), but not significantly so between years when compared to alpha values of the months (two-way ANOVA:  $F_{1:20} = 0.48$ ,  $P > 0.05$ ). Abundance was significantly higher in the wet season ( $N = 9737$ ) than the dry season ( $N = 3613$ ) (two-way ANOVA:  $F_{1:20} = 8.58$ ,  $P < 0.01$ ), and when species richness of wet ( $S = 271$ ) and dry ( $S = 228$ ) seasons was rarefied, we found no difference (Fig. 4). Although alpha was lower in wet (51.73) than in dry season (54.13), diversity did not vary significantly between seasons (two-way ANOVA:  $F_{1:20} = 0.13$ ,  $P > 0.05$ ). Six of the 24 months (i.e. Feb. 2010, Mar. 2010, Mar. 2011, Nov. 2011, Apr. 2010, and Apr. 2011) did not fit a log series model. Monthly abundance correlated significantly with temperature  $\rho = 0.65$ , 22 df,  $P < 0.001$ , but not with rainfall, nor did species richness and Fisher's alpha (all  $P > 0.05$ ). Monthly abundance in 2010 and 2011 correlated significantly with temperature, even after Bonferroni correction (Holm 1979) – 2010:  $\rho = 0.67$ , 10 df,  $P < 0.05$ ; 2011:  $\rho = 0.61$ , 10 df,  $P < 0.05$ . Fisher's alpha and species richness of each year did not correlate with temperature and rainfall, nor did abundance and rainfall (all  $P > 0.05$ ).

**Table 2.** Number of specimens (N), species (S) and number of sampling nights (SN) in different periods and altitudinal levels.

|          | Lowland |     |    | Submontane |     |    | Montane |     |    | Total |     |     |
|----------|---------|-----|----|------------|-----|----|---------|-----|----|-------|-----|-----|
|          | N       | S   | SN | N          | S   | SN | N       | S   | SN | N     | S   | SN  |
| Wet 2010 | 567     | 112 | 17 | 1239       | 116 | 12 | 3504    | 196 | 20 | 5310  | 236 | 49  |
| Dry 2010 | 447     | 106 | 17 | 477        | 103 | 12 | 967     | 120 | 23 | 1891  | 188 | 52  |
| Wet 2011 | 378     | 108 | 15 | 546        | 113 | 10 | 3503    | 182 | 22 | 4427  | 230 | 47  |
| Dry 2011 | 405     | 108 | 18 | 391        | 88  | 12 | 926     | 113 | 23 | 1722  | 188 | 53  |
| 2010     | 1014    | 151 | 34 | 1716       | 147 | 24 | 4471    | 206 | 43 | 7201  | 255 | 101 |
| 2011     | 783     | 148 | 33 | 937        | 137 | 22 | 4429    | 199 | 45 | 6149  | 252 | 100 |
| Wet      | 945     | 148 | 32 | 1785       | 152 | 22 | 7007    | 230 | 42 | 9737  | 271 | 96  |
| Dry      | 852     | 147 | 35 | 868        | 135 | 24 | 1893    | 155 | 46 | 3613  | 228 | 105 |
| Total    | 1797    | 195 | 67 | 2653       | 185 | 46 | 8900    | 242 | 88 | 13350 | 288 | 201 |

The two-way repeated measurements ANOVA comparing seasons along years and altitudinal levels (Fig. 5a) revealed differences in specimens numbers were marginally significant among seasons ( $F_{1:11} = 4.68$ ,  $P = 0.053$ ), and abundance varied significantly among elevations ( $F_{2:22} = 28.47$ ,  $P < 0.001$ ), i.e. abundance was significantly higher in

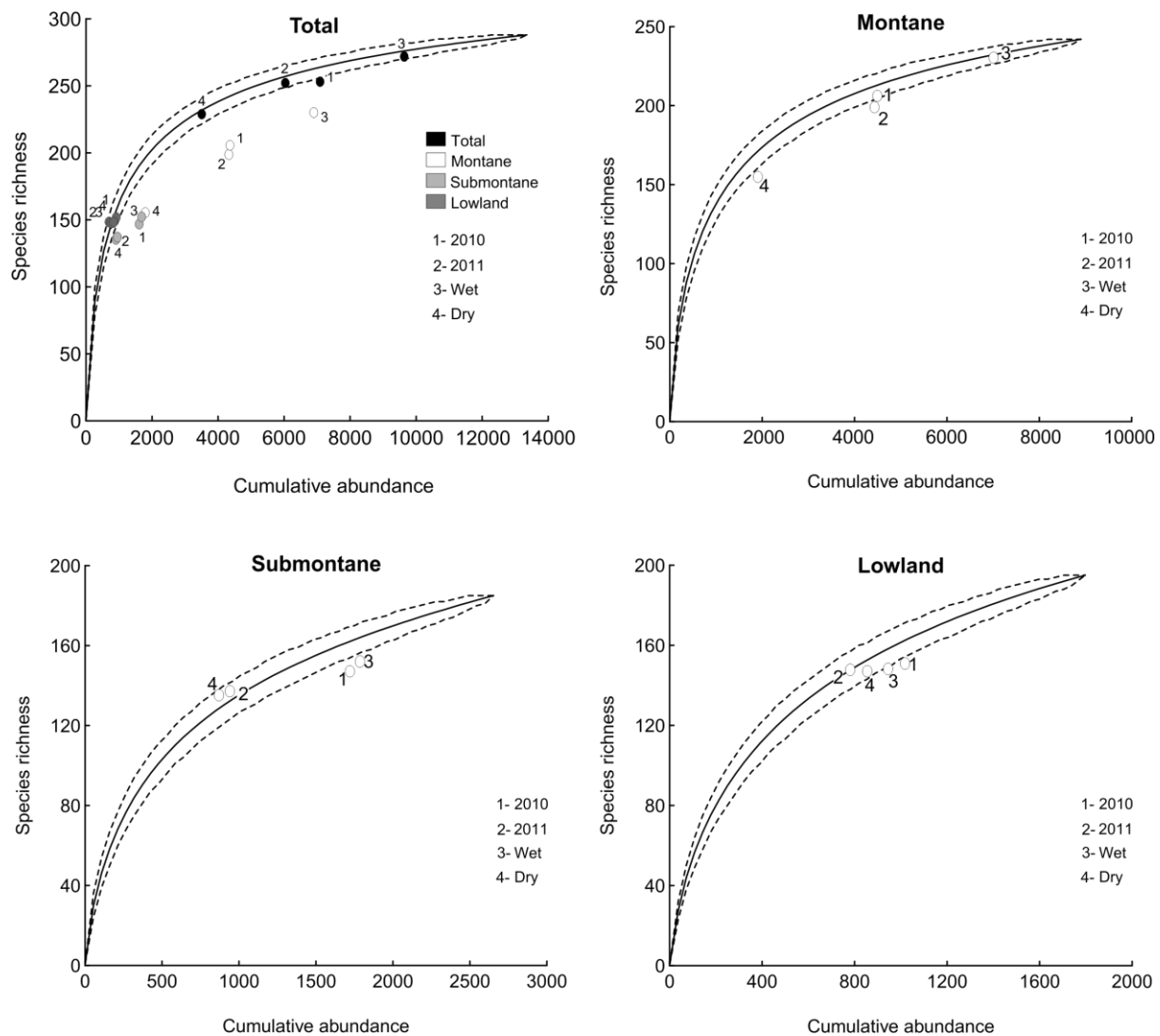
Montane during the wet season (Fig. 5a). Overall abundance did not differ significantly between Lowland and Submontane ( $P > 0.05$ ), but differed between Montane and other elevations ( $P < 0.01$ ). The two-way repeated measures ANOVA revealed a significant interaction between seasons and elevations ( $F_{2:22} = 5.42$ ,  $P < 0.05$ ), i.e. the wet season of 2010 and 2011 were markedly higher in Montane, but not in Lowland and Submontane (Table 2 and Fig. 5a). The assumption of homogeneity of variances were not significant (Levene test – Seasons: Test Statistic = 1.33,  $P > 0.05$ ; Elevation: Test Statistic = 2.43,  $P > 0.05$ ; Interaction: Test Statistic = 1.33,  $P > 0.05$ ).



**Figure 3.** Monthly abundance (A) and species richness (B) recorded during the sampling period in the three elevations. Numbers in the x axis represents months, from February 2010 to January 2012.

The two-way repeated measures ANOVA comparing seasons along years and elevations (Fig. 5b) revealed that diversity did not change significantly among seasons ( $F_{1:22} = 0.003$ ,  $P > 0.05$ ), but did change along elevations ( $F_{2:22} = 4.04$ ,  $P < 0.05$ ), with a significant overall difference between Submontane and the other elevations; there was no interaction

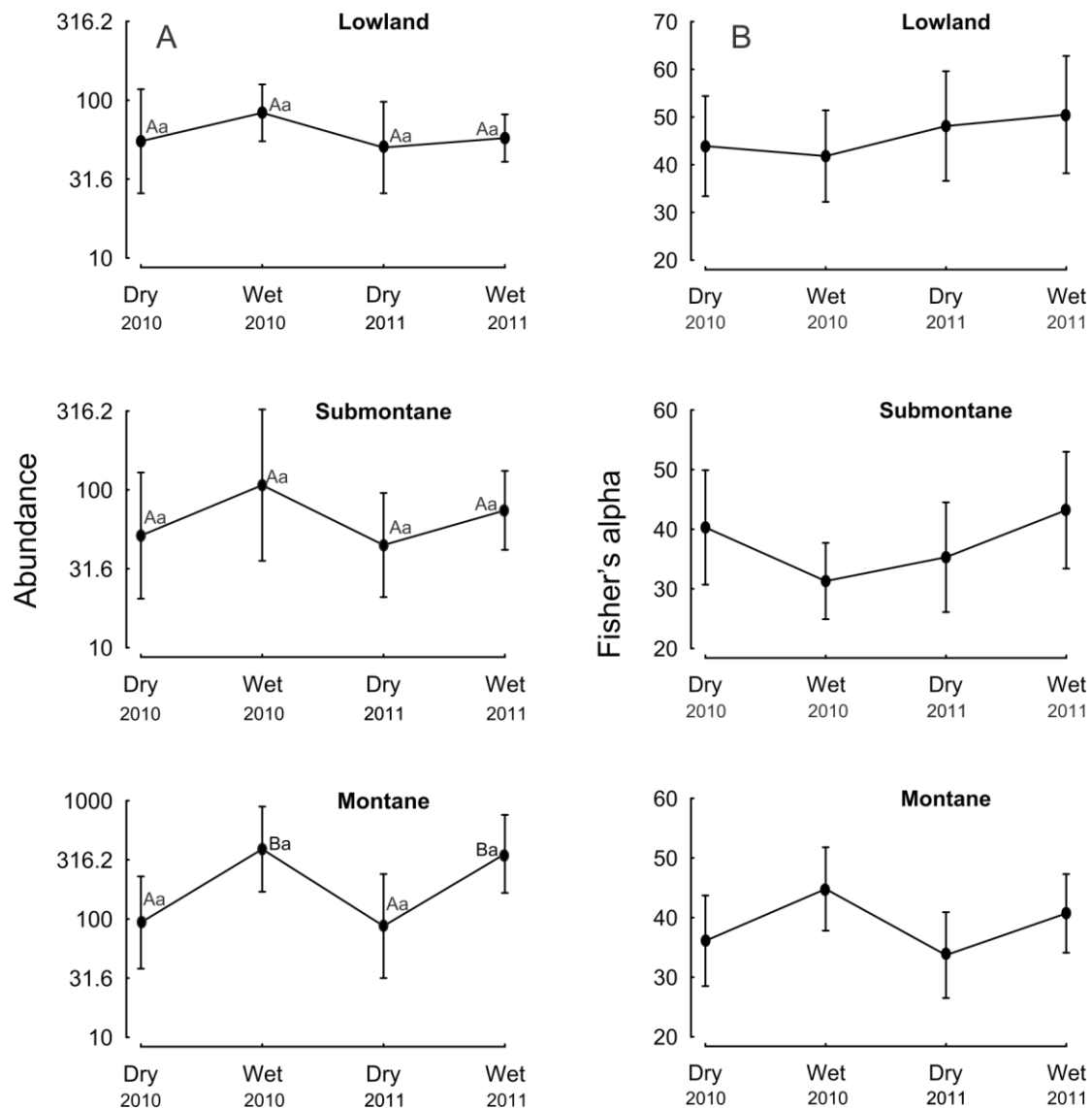
between seasons and elevations ( $F_{2:22} = 0.42$ ,  $P > 0.05$ ). Three of the 13 data sets did not fit a log series model (Submontane - dry season, 2011; Montane - wet season, 2010, and wet season, 2011), and the Levene tests were all not significant (Seasons: Test Statistic = 2.86,  $P > 0.05$ ; elevations: Test Statistic = 0.0004,  $P > 0.05$ ; Interaction: Test Statistic = 0.93,  $P > 0.05$ ).



**Figure 4.** Rarefaction analysis based upon 10,000 re-samples of the total data set, Lowland, Submontane and Montane data sets and its 95% confidence intervals.

Rarefaction of total data set indicated that species richness was higher in Lowland than Submontane and Montane (Fig. 4), and that total and Lowland species richness did not differ between years and seasons, except for 2010 when richness was higher in Lowland than total species richness (Fig. 4). Rarefaction of the Montane data set indicated that richness was significantly higher in 2010 than 2011, and in the wet season rather than in dry season (Fig.

4). Differently, richness was higher in 2011 and in the dry season in Lowland and Submontane (Fig. 4).



**Figure 5.** Abundance and diversity recorded during dry and wet season of 2010 and 2011 in the three elevations. (A) Mean abundance: data was log transformed ( $\log_{10}$ ) to reduce variances. Upper case letters are differences between elevations, lower case letters are differences between seasons. (B) Fisher's alpha of the log series. Error bars are 95% confidence intervals. See text for details.

### 3.2 Spatiotemporal dynamics of dominant species

The influence of elevation and seasons was tested separately for the 20 species with a hundred or more individuals (Table 3). However, four species nearly restricted to one elevation were represented by more than a hundred individuals. Three were restricted to

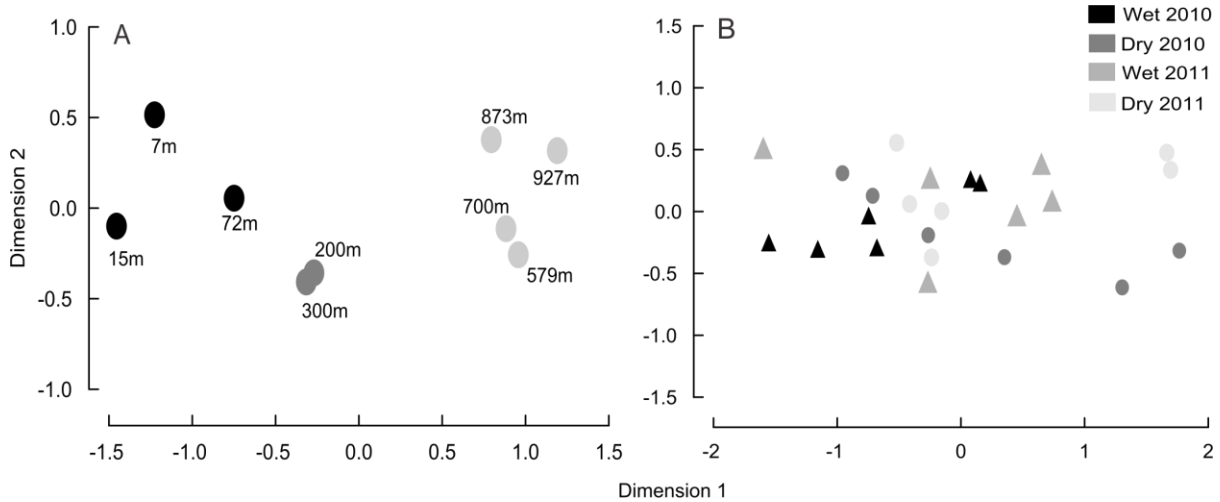
Montane habitat (*Phaegoptera fusca*, *Erruca sanguipuncta* and *Ichoria tricineta*), with *P. fusca* and *I. tricineta* having one individual in Submontane habitat. There were no species restricted to Lowland or Submontane habitats, but *Ochrodota pronapides* had only one individual recorded in Montane, 61 in Submontane and 33 in Lowland habitat. Between wet and dry seasons, only *I. tricineta* was significantly more abundant during the wet season ( $t = 3.12$ ,  $df = 3.81$ ,  $P < 0.05$ ).

**Table 3.** Given are results of the two-way ANOVA tests for the 20 species with more than 100 specimens, considering differences in abundance between the three altitudinal levels (Elevation) and wet and dry seasons (Seasons). Species are organized from the most to least abundant. See text for more details. \* $<0.05$ , \*\* $<0.01$ , \*\*\* $<0.001$ .

| Species                   | F <sub>2,12</sub> (Elevation) | F <sub>1,12</sub> (Season) | F <sub>2,12</sub> (Interaction) |
|---------------------------|-------------------------------|----------------------------|---------------------------------|
| <i>Agylla</i> spJAT01     | NS                            | 19.82***                   | NS                              |
| <i>Agylla</i> spJAT02     | 7.04**                        | 5.77*                      | NS                              |
| <i>Agylla</i> spJAT03     | 13.82***                      | NS                         | NS                              |
| <i>Melese</i> spJAT01     | 21.73***                      | NS                         | NS                              |
| <i>Agylla polysemata</i>  | 25.83***                      | NS                         | 8.17**                          |
| <i>Agylla</i> spJAT09     | NS                            | NS                         | NS                              |
| <i>Symphlebia perflua</i> | 6.53*                         | 10.42**                    | NS                              |
| <i>Melese chozeba</i>     | 15.14***                      | 6.33*                      | NS                              |
| <i>Cosmosoma centrale</i> | NS                            | 5.68*                      | NS                              |
| <i>Agylla</i> spJAT08     | NS                            | NS                         | NS                              |
| <i>Dysschema amphissa</i> | 7.61**                        | NS                         | NS                              |
| <i>Melese</i> spJAT07     | 66.18***                      | 12.1**                     | NS                              |
| <i>Eucereon apicalis</i>  | 15.21***                      | NS                         | NS                              |
| <i>Cissura decora</i>     | 5.7*                          | NS                         | NS                              |
| <i>Trichromia</i> spJAT01 | NS                            | NS                         | NS                              |
| <i>Aclytia</i> spJAT01    | NS                            | NS                         | NS                              |
| <i>Erruca hanga</i>       | 16.17***                      | NS                         | NS                              |
| <i>Melese castrena</i>    | 5.73*                         | NS                         | NS                              |
| <i>Virbia divisa</i>      | 21.62***                      | 22.08***                   | NS                              |
| <i>Amaxia hebe</i>        | 4.24*                         | NS                         | NS                              |

The individual two-way ANOVA tests for the 20 species with a hundred or more individuals indicated that four species were not influenced by elevation or seasonality (Table 3). Although there was no significant difference between elevations in three of the six *Agylla* species listed in Table 3, the abundance of the *Agylla* species was considerably higher in Montane than in other elevations. Abundance differed significantly between elevations and seasons in five species, but a significant interaction between both factors was found only for *Agylla polysemata*. The only species in which abundance was significantly higher during dry

season was *Melese* spJAT07, whereas species abundance in all other species was higher in the wet season (Table 3).



**Figure 6.** Nonmetric multidimensional scaling (NMDS) ordinations using Bray-Curtis dissimilarities. Given are only two dimensions. (A) Ordination using data of individual sites (stress: 0.0103); black circles: Lowland; dark gray circles: Submontane; light gray circles: Montane. (B) Ordination using monthly data of wet (triangles) and dry (circles) seasons of 2010 and 2011 (stress: 0.1102).

### 3.3 Spatiotemporal dynamics of community composition

The NMDS plot for the nine sampling sites revealed a clear segregation between the three elevations (Fig. 6A), and it was confirmed by ANOSIM (Table 4). Furthermore, the ANOSIM results revealed that community composition was different between wet and dry season, but not between the same season in different years, although it was not possible to distinct this pattern in NMDS analysis (Fig. 6B). Community composition differed significantly in the three elevations during the wet season, but Lowland and Submontane did not differ during the dry season (Table 4). Finally, the NMDS indicated a positive correlation between elevations and the scores of the first axis of sampling sites ( $r = 0.95$ , 7df,  $P < 0.001$ ).

## 4.0 Discussion

### 4.1 Does abundance, species richness and diversity change with elevation and seasons?

Insects with broad altitudinal distributions face the general problem of adapting their life histories to compensate for deteriorating environmental conditions for growth and

reproduction, particularly decreasing temperatures with increasing elevation (Hodkinson 2005). We found a steep increase in abundance from Lowland to Montane (Figs 3A), whereas we expected a decline in Submontane and Montane coldest climate (i.e. we found an average difference of 3.7°C, see Fig. 1 for details). As a consequence of the higher temperatures in Lowland one might expect species to have a shorter developmental period with more than one generation per year and, therefore, a higher abundance compared to the elevations, as observed for British butterflies (Pollard & Yates 1993). One potential explanation for this reverse pattern might be that abundance, and also species richness, would be controlled by the “mid-domain effect” where species ranges overlap increasingly toward the center of the gradient, thus resulting in a higher abundance and species richness (Colwell & Lees 2000, Zapata et al. 2003). Unfortunately, we did not sample over the complete local altitudinal gradient (0 – 1500m) to test this idea. However, the mid-domain effect has been reported for moths along altitudinal gradients (Brehm et al. 2007), and in the Atlantic Forest arctiines it is probable that species diversity declines above 1000m due to lower temperatures. It is worth noting that other abiotic factors like low CO<sub>2</sub>, increased UV exposure and wind, and biotic factors like competition, predation, parasitism and intrinsic characteristics of each species can also affect insect diversity along altitudinal gradients (Hodkinson 2005).

**Table 4.** Analysis of Similarities (ANOSIM) based on Bray-Curtis dissimilarities. Given are several comparisons between altitudinal levels and seasons regarding beta diversity. P values in bold were not significant.

| Comparison            | R    | P            | Comparison | R    | P            | Comparison | R    | P            |
|-----------------------|------|--------------|------------|------|--------------|------------|------|--------------|
| Altitude:             |      |              |            |      |              |            |      |              |
| LO vs. SM             | 0.23 | 0.001        |            |      |              |            |      |              |
| LO vs. MO             | 0.61 | 0.001        |            |      |              |            |      |              |
| SM vs. MO             | 0.48 | 0.001        |            |      |              |            |      |              |
| Season:               |      |              | Dry 2010:  |      |              | Dry 2011:  |      |              |
|                       |      |              | LO vs. SM  | 0.12 | <b>0.100</b> | LO vs. SM  | 0.10 | <b>0.184</b> |
|                       |      |              | LO vs. MO  | 0.57 | 0.002        | LO vs. MO  | 0.45 | 0.004        |
| Dry 2010 vs. Dry 2011 | 0.05 | <b>0.077</b> | SM vs. MO  | 0.40 | 0.005        | SM vs. MO  | 0.48 | 0.012        |
| Dry 2010 vs. Wet 2010 | 0.06 | 0.047        |            |      |              |            |      |              |
| Dry 2010 vs. Wet 2011 | 0.10 | 0.009        | Wet 2010:  |      |              | Wet 2011:  |      |              |
| Wet 2010 vs. Dry 2011 | 0.18 | 0.007        | LO vs. SM  | 0.19 | 0.038        | LO vs. SM  | 0.35 | 0.009        |
| Wet 2010 vs. Wet 2011 | 0.03 | <b>0.146</b> | LO vs. MO  | 0.68 | 0.006        | LO vs. MO  | 0.86 | 0.006        |
| Wet 2011 vs. Dry 2011 | 0.17 | 0.002        | SM vs. MO  | 0.33 | 0.007        | SM vs. MO  | 0.63 | 0.005        |

Another important determinant is seasonal phenology and distribution of host-plants. It is known that Arctiine larvae are “specialized generalists” (Singer & Bernays 2009) that may feed on several non-related host-plants, but required pyrrolizidine alkaloids (PA) to use



as chemical defenses and in male courtship. Thus, it is probable that host-plants distribution and phenology could influence Arctiine diversity patterns along altitudinal gradients and broad scale geographic gradients. Unfortunately neither thorough arctiine host-plant lists nor altitudinal distributions of PA plants are available for the Neotropical region.

It is clear that higher temperature has a stronger effect on Montane-dwelling insects than Lowland and Submontane insects, since there was a significant difference in abundance of wet seasons in Montane and the other elevations (Fig. 5a). However, dry seasons were not significantly different between altitudinal levels. Therefore, differently from higher elevation temperate insects that usually enter overwinter diapause (Hodkinson, 2005), Atlantic Forest Montane-dwelling moths develop throughout the year with little restriction. The higher abundance during the wet season in Montane might be attributed to an incoming of moths from Lowland and Submontane, probably because the difference of temperature between Lowland and Montane. In fact, this patterns has been recorded also for butterflies on the seaward slope of the coastal mountains of Serra do Mar, but differently from arctiins there was also a movement back during the dry season (see references at Bown and Freitas, 2000).

We found differences between total wet and dry seasons, where significantly more individuals were sampled during wet season ( $N = 9737$ ) than dry season ( $N = 3613$ ). This is in contrast to a study of Montane rainforest in Southern Ecuador by Hilt et al. (2007) who assessed diversity of arctiines in different successional stages and seasons, but found no significant abundance differences between seasons. Another study conducted in the same study area (Süssenbach, 2003) found that arctiine abundance was higher during dry than the wet season. It is widely known that temperate and tropical insect communities are seasonal (Janzen, 1973; Wolda, 1978, 1992; Pinheiro et al., 2002). Neotropical butterfly abundance is usually higher during wet seasons (DeVries et al., 1997), and this might be expected because the onset of rainfall triggers budbreak and flowering in many plants, thus making resources available for larvae and adults Lepidoptera (Hilt et al. 2007). Therefore, one potential explanation for the discrepancy between our study and other studies on arctiine diversity (Süssenbach, 2003, Hilt et al., 2007) is that our two year sampling effort was evenly distributed among both dry and wet seasons, whereas in the other works sampling was insufficient or unevenly distributed along wet and dry seasons.

Fisher's alpha indicated that diversity was equally higher in Lowland and Montane, but rarefaction analysis suggested that richness was higher in Lowland than Montane. Therefore, according to the rarefaction analysis, richness is higher in Lowland rather in the mid-elevation (Montane), counteracting the mid-domain effect theory. Fisher's alpha did not

change along seasons in any elevation, but rarefaction analysis revealed that species richness was higher during the wet season in Montane, and during the dry season in the other elevations. Further studies are needed to clarify seasonal movements of species from Lowland to a higher elevational range, and to determine the influence of nearby Araucaria Forests in Montane species richness.

The significant difference of species richness between years revealed by the rarefaction analysis might be explained by the slightly higher, but not significant, difference of temperature and rain fall during the wet season of 2010 (means: 21.35°C, 10.11mm) and 2011 (means: 20.63°C, 7.13mm), (temperature:  $t = 0.61$ , 8.72 df,  $P > 0.05$ ; rainfall:  $t = 1.6$ , 6.86 df,  $P > 0.05$ ). Therefore, when assessing diversity of arctiines in nearby areas of Atlantic Forest we recommend that sampling take place along two or more years.

#### 4.2 The influence of dominant species

As expected, most of dominant species were more abundant in Montane, but *Melese* spJAT01, *Melese* spJAT07 and *Virbia divisa* were more abundant in Submontane, probably because of the flight activity constraints imposed by the coldest climate of Montane. Furthermore, all species with significant difference between seasons were more abundant during the wet season, excluding *Melese* spJAT07. The fact that two species of *Agylla* were more abundant during the wet season is very similar to the results of Hilt et al. (2007), where also two species of *Agylla* were significantly more abundant during the wet season.

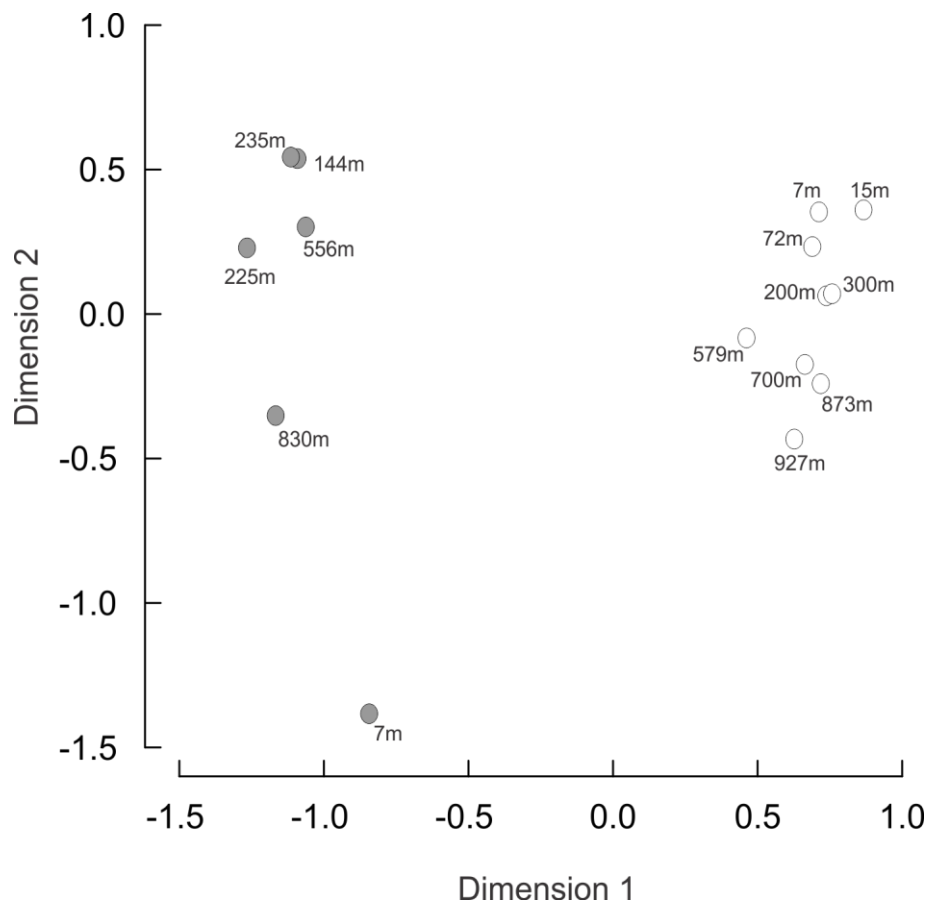
#### 4.3 Beta diversity patterns

Temporal  $\beta$  diversity patterns showed that community composition does not change during the dry season in Lowland and Submontane, but it does between Montane and the other elevations (Table 4). Three hypothesis might explain these patterns: (1) as temperature is lower in Montane there would be a reduced number of specimens attracted to light traps, and a consequently change in species composition; (2) host plant species phenology could be acting during the dry season to maintain a different species composition in Montane; (3) there would be an incoming of species from higher elevations and/or nearby Araucaria forest in Montane during the dry season. Seasonal variation in species composition of Neotropical arctiines within the elevational gradient exposed here has never been recorded before. Available data were recorded from higher altitude in the rainforest of Southern Ecuador (Hilt et al., 2007, Süssenbach, 2003), and indicated no clear seasonal patterns for that region, although the authors assumed that the sampling period was insufficient.

The distinction between Lowland and Montane species composition in the Atlantic Forest has been documented before based on Museum data and published species lists (Ferro & Mello, 2011). However, we have demonstrated that community change gradually from Lowland to Montane, as recorded for arctiins from a higher elevational gradient in Southern Ecuador (Süssenbach, 2003). Besides the obvious environmental constraints caused by elevation, one can expect that plant community composition also can affect  $\beta$  diversity of moths along elevational gradients. In fact, Brehm et al. (2003b) found that both geometrid moth and tree ensembles change gradually along altitude. Although tree ensembles ordination studies are unavailable for our study area, it is known that vascular epiphytes species composition do change gradually from 400 to 1,000m a.s.l. (Blum et al., 2011), thus it is highly probable that  $\beta$  diversity of trees also change gradually along our altitudinal transect. However, considering that many arctiini species are polyphagous, but still require Pyrrolizidine Alkaloids from particular plant species, concomitant studies on distribution of arctiine moths and PA host plants along altitudinal gradients could be useful to determine the factors affecting community composition of arctiins along altitude. Similarly, the host identification of Lithosiini caterpillars which feed on lichens and mosses and the distribution of these hosts along elevational gradients would also be of great help.

The availability of a previous work (Teston & Corseuil, 2004) where alpha diversity of the tribe Arctiini was studied in six locations (three in the Atlantic Forest and three in Pampa Biome) in the southernmost state of Brazil (Rio Grande do Sul), with an almost identical sampling effort and collecting methods we used, allowed us to compare  $\beta$  diversity of Arctiini of southern Atlantic Forest. As expected, because of the geographical distance between Rio Grande do Sul and Paraná State, the first dimension of the NMDS ordination revealed a clear segregation between both communities (Fig. 7), what was confirmed by ANOSIM ( $R = 0.5642$ ,  $P < 0.001$ ). Similarly, the second dimension showed a clear segregation of our sampling sites according to altitude (correlation between the second scores and elevation:  $r = 0.98$ , 7 df,  $P < 0.001$ ), but the same did not happen with the sampling sites of Teston and Corseuil (2004) (correlation between the second scores and elevation:  $r = -0.23$ , 4 df,  $P > 0.05$ ), as illustrated in Figure 7. One probable explanation for this unexpected pattern would be that sampling sites were ordinated according to vegetation composition, since it is known that arctiine faunal composition in the southernmost part of the Atlantic Forest is determined by different vegetation types (Ferro & Teston 2009). Therefore, it worth to note that the relationship between moths species composition and elevation can yield meaningful results only when it is analyzed in a relatively small spatial scale (a mountain, in

our case), whereas in a broad geographical scale, as in the case of Teston and Corseuil (2004), the results may reflect other factors affecting  $\beta$  diversity rather than elevation. However, when considering several records of species occurrence, as in the meta-analysis of Ferro and Melo (2011), it is possible to obtain meaningful results.



**Figure 7.** Nonmetric multidimensional scaling (NMDS) ordinations using Bray-Curtis dissimilarities (Arctiini data only) between sampling sites of Teston and Corseuil (2004) (gray circles) and this study (white circles) (stress = 0.2255). Given are only two dimensions. The numbers are altitudes in meters (m) above sea level.

## 5. Conclusion

This work showed that arctiine abundance increase with elevation with a markedly difference between Montane and the other elevations, and that abundance is higher in Montane during the wet season. This pattern probably is the result of a combination of biotic and abiotic factor affecting abundance along the elevational gradient. Although species richness and abundance are higher in Montane the two measures used (rarefaction analysis

and Fisher's alpha) indicated that diversity is higher in Lowland, although Fisher's alpha showed no difference between Lowland and Montane. Therefore when we consider species richness as a diversity measure, the mid-domain effect is corroborated, but when we consider species richness and abundance in a single diversity measure mid-domain effect is refused. Further studies are needed to determine diversity in the Atlantic Forest at higher elevations to compare with the elevational range studied here. Arctiins ensembles change gradually from Lowland to Montane forest, but Lowland and Submontane are more similar during the dry season than Montane. This pattern might be the result of the incoming o moths from lower elevation or from nearby Araucaria forests. Mark recapture studies are needed to determine seasonal movements of arctiins in the study area. The comparison of species composition changing between our study and the study of Teston and Corseuil (2004) indicated that community composition can be attributed to elevation when we consider a mountain region where distance between two point within steep altitudinal range are short (as in our case), but when we consider longer distances, as in the case of Teston and Corseuil (2004), other factors may influence  $\beta$  diversity.

#### Aknowledgements

We would like to thank the Brazilian government funding agencies CNPq (Conselho Nacional de Desenvolvimento Cietífico e Tecnológico, process number 141142/2009-0) and CAPES (Comissão de Aperfeiçoamento de Pessoal de Nível Superior, process number 5708-11-7) for the first author's scholarships. We gratefully acknowledge the University of New Orleans (USA) for the support during the period when the first author visited this institution and to Dr. Michel Laguerre (Institut Européen de Chimie et Biologie, France) for the identification of the Lithosiini species. Finally, we especially thank all the inhabitants of the Serra da Graciosa for the great help during the course of this study.

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### **Chapter 3: Assessing Tiger moths diversity in Brazilian Atlantic Forest using DNA barcodes**

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**Abstracts:** DNA barcoding is a molecular technique used to discriminate biological species assuming that intraspecific genetic divergence is lower than interspecific divergence. For any given species, it also requires that a library of DNA barcodes is assembled with samples from its entire geographical range. As part of a two-year biodiversity study of tiger moths (Lepidoptera: Erebidae) along an elevational transect in southern Brazilian Atlantic Forest, we built a reference collection and tissue samples of the specimens were submitted to Canadian Centre for DNA barcoding. We obtained 1100 barcode sequences for 290 morphological species, of which 136 were identified to species and 85 to genus. This information is part of the global library of DNA barcodes (<http://www.barcodinglife.com/>) and can be used to identify specimens from the Atlantic Forest. We also compared the correspondence between DNA barcoding and morphology as means for species discrimination. Morphology and DNA barcoding distinguished 161 species equally well, but the results cannot be readily interpreted as low performance of DNA barcoding because we were not able to assess genitalic morphology. Our results can be considered satisfactory considering that an integrative taxonomical approach is usually required to discriminate species of Arctiinae and that we had a reduced number of sequences per species. Further morphological studies are needed to determine the correspondence between species recognized by morphology and DNA barcoding.

**Key words:** morphospecies, library of DNA barcodes, species richness, Paraná, Arctiidae.

## 1. Introduction

The identification of animal species using a fragment with 648-bp of the mitochondrial gene cytochrome *c* oxidase I (COI), known as DNA barcoding (Hebert et al. 2003a, b), has attracted much attention and controversy (e.g. Will and Rubinoff, 2004; Marshall, 2005; Ebach and Holdrege, 2005; Schindell and Miller, 2005). The implementation of the Consortium for the Barcode of Life (<http://www.barcodeoflife.org>) has promoted several studies to test the reliability of DNA barcoding to discriminate species in different animal taxa such as birds (Kerr et al., 2007), fishes (Steinke et al., 2009), mammals (Clare et al., 2011) and spiders (Berrett and Hebert, 2005) with mostly favorable results.

The underlying assumption for the effective use of DNA barcoding as a taxonomic tool is that intraspecific genetic distance is lower than interspecific distance, i.e. the so-called DNA barcoding gap (Hebert et al. 2003a; Wiemers and Fiedler, 2007). To determine whether a DNA barcoding gap exists for a specific taxon, and the size of this gap, it is necessary assemble a library of DNA barcodes. If such gap exists and the species coverage is broad, this library can be used to compare sequences between taxa, and to identify specimens of unknown identity (Hajibabaei et al., 2005). However, two important issues must be considered when assembling a DNA barcode library: first, for widespread species, it is important to obtain samples (individuals) throughout their geographical range so that intraspecific COI sequence variation will be captured; second, the taxonomy of target organisms must be well resolved, otherwise the initial goal of species identification would be lost (Meyer and Paulay, 2005).

Many projects/campaigns have been undertaken to build DNA barcode libraries for different animal taxa such as birds (<http://www.barcodingbirds.org/>), fishes (<http://www.fishbol.org/>) and mammals (<http://www.mammaliabol.org/>), but the Lepidoptera (moths and butterflies) is the taxon with the largest library in the Barcode of Life database ([www.barcodinglife.com](http://www.barcodinglife.com)), with 72,739 species represented by 684,019 barcoded specimens. Several projects have contributed to that progress (see a list in <http://www.lepbarcoding.org/>), especially the biodiversity inventory of “Area de Conservación Guanacaste” in Costa Rica where a massive barcoding campaign was undertaken for moths, butterflies and their parasitoids (Janzen et al., 2005; Smith et al., 2008; Janzen et al., 2009). Although many taxa within Lepidoptera have been sampled all over the world ([www.boldsystems.org](http://www.boldsystems.org), Ratnasingham and Hebert, 2007) some regions that may harbor several unrecorded species

remain underrepresented. The inclusion of such species in the barcode library may reveal hidden biodiversity and will contribute to library improvement.

Tiger moths (Erebidae: Arctiinae) are small to medium size moths with approximately 11,000 described species distributed worldwide (Watson and Goodger, 1986). The number of barcode sequence records for arctiines from South American countries is considerably smaller when compared to North and Central America, and are concentrated in the eastern region (Andes) ([www.barcodinglife.com](http://www.barcodinglife.com)). The Atlantic Forest occupies a large portion of the Brazilian coastal land with approximately 29° latitudinal range, extending from the northeast to the south, and it is considered a high priority conservation hotspot (Myers *et al.*, 2000; Brummit & Lughadha, 2003). The implementation of a biodiversity survey along an elevational transect in a conserved patch of Atlantic Forest of southern Brazil between 2010 and 2012 (chapters one and two) allowed us to establish, in 2010, a collaborative project with the Canadian Centre for DNA Barcoding, entitled “Lepidoptera of Serra do Mar”. One of the purposes of this project was to contribute to the improvement of the DNA barcode library for arctiines with samples of specimens collected from that study area.

Additionally, the objectives of this work were: (1) to report the results of the Lepidoptera of Serra do Mar project and discuss its relevance to Barcode of Life database and Arctiinae taxonomy; (2) to evaluate the correspondence between species diagnosed by DNA barcoding and morphology using the DNA barcode sequences in the project; (3) to compare species richness revealed by DNA barcoding and morphology in the sampled elevational transect and discuss the use of DNA barcoding in our biodiversity study.

## **2. Material and Methods**

### **2.1 Sampling and taxonomic assignment**

We used automatic light traps model Pennsylvania (Frost 1957) equipped with UV lights to sample moths from 14 sites (Table 1) located along an elevational transect through “Serra da Graciosa” in southern Brazilian Atlantic Forest, Paraná State (see chapters one and two for a map with sampling site locations). We attached a 2 L plastic bucket filled with 90% ethanol to the base of the trap (Specht & Corseuil, 2002; Teston & Corseuil, 2004) to collect the moths and to prevent DNA degradation (Szinwelski *et al.*, 2012). Traps were run during the night and samples were brought to the laboratory in the next morning where arctiines were sorted.

We build an Arctiinae reference collection with at least three specimens of each morphological species, and singletons and remaining specimens were stored in envelopes. Species of Arctiini were identified by J.A.T. based on Brazilian collections cited in Teston and Corseuil (2002, 2003a, b). Arctiini specimens identified to genus-level were assigned to five subtribes following Teston and Corseuil (2002). Where genus level identification was not possible, specimens were assigned to subtribes based on external morphology and color pattern. Lithosiini specimens were identified by Dr. Michel Laguerre based on the collections of the Natural History Museum (London) and Muséum National d'Histoire Naturelle (Paris). Subtribal classification for Lithosiini specimens was not possible due to unavailability of Neotropical species checklists. Higher-level classification followed Jacobson & Weller (2002), Zahiri et al. (2011), Zahiri et al. (2012).

## 2.2 DNA extraction and amplification

Tissue samples consisting of one small leg segment with 2-5mm length were removed from specimens in our reference collection and deposited in 96-well plates prefilled with 30 µl of 95% ethanol. All instruments used to remove leg tissues were cleaned in 90% ethanol after handling each specimen. DNA was extracted from tissue samples following standard protocols (Ivanova *et al.* 2006, Ivanova *et al.* 2012). PCR amplification, product checking, PCR cycle sequencing, and sequencing followed standard protocols employed at the Canadian Centre for DNA Barcoding (Ivanova and Grainger 2012a,b). All specimen collection data, sequences, PCR and sequencing primers, and trace files are available through the Barcode of Life Data Systems (Ratnasingham and Hebert 2007) under project name “Lepidoptera of Serra do Mar”.

## 2.3 Data analysis

Only high-quality sequences of at least 600 bp and containing less than 1% missing nucleotides (Ns) were retained for data analysis to reduce intraspecific variations due to sequence length (Ratnasingham and Hebert, 2007). The sequences were aligned using BOLD Aligner (Amino Acid Based Hidden Markov Model). The Neighbor Joining phenogram and barcode gap analysis (distance from the nearest neighbor) were performed using tools available in the Bold Systems web site; in both analysis we choose Kimura 2-Parameter (K2P) as the distance model. We used the Neighbor Joining phenogram and the barcode gap analysis to examine whether the species discriminated by DNA barcoding corresponded to our pre-defined morphological species. Thereafter, pairwise distances within and between the



species revealed by DNA barcoding were recalculated using the program Mega 5 (Tamura et al., 2011) and we produced a detailed species list with the rearrangements in the species identities. Finally, we reassessed external morphology of the species to examine the sources of disagreement of DNA barcoding and morphology to explain the rearrangements of the species.

We produced two species accumulation curves in order to compare species richness revealed by external morphology and DNA barcoding. First, the abundance data recorded during the biodiversity study based on morphological species recognition. Second, we produced a species accumulation curve based on taxa recognized by their DNA barcode sequences.

### 3. Results

#### 3.1 Data in the project Lepidoptera of Serra do Mar

We obtained 14026 individuals and 294 species of Arctiinae along the elevational transect in Serra da Graciosa (Table 1, see chapter one for a species list). A total of 1117 samples of 290 recognizable entities were submitted to Canadian Centre for DNA Barcoding, between March 2010 and March 2012, representing 7.93% and 98.64% of total abundance and species richness recorded in the collections, respectively. Of the 290 entities, 136 were identified to species, 85 to genus, and 26 to tribe/subtribe (Appendix 1III). DNA extraction and sequencing were successful for most samples, and only 17 failures were recorded. Two sequences were shorter than 600 bp (Sample IDs: MMZ0524 [*Illice* sp. ML03] 597 bp and MMZ1041 [*Rhynchopyga meisteri*] 598 bp), 39 sequences were between 604 bp and 657 bp long, and the remaining 1059 sequences were 658 bp. No contamination or stop codons were detected.

The project Lepidoptera of Serra do Mar is the eighth largest project in the Bold systems web site in the number of sequences of Arctiinae and account for 3.29% and 8.05% of total DNA barcode sequences and species of Arctiinae in the Bold Systems database, respectively. The number of DNA barcode sequences for Arctiinae in Brazil increased from 143 to 1243 after our specimens were included. A total of 2117 scaled photographs of dorsal and ventral views are available in the Bold Systems website representing all species with DNA barcode sequences in the Lepidoptera of Serra do Mar Project. All data in the project are integrated in the identification engine and taxonomy browser of the Bold Systems database ([www.barcodinglife.com](http://www.barcodinglife.com)).

**Table 1.** Species richness and abundance of Arctiinae recorded along an elevational transect in southern Brazilian Atlantic Forest (Serra da Graciosa), and number of species with DNA barcode sequences and number of sequences (individuals) for each sampling site recorded in the project Lepidoptera of Serra do Mar.

| Sampling sites | Elevation | Species richness | Number of species with DNA barcode sequence | Species abundance | Number of specimens with DNA barcode sequence |
|----------------|-----------|------------------|---|-------------------|---|
| 1              | 7m        | 109              | 47  | 434               | 66  |
| 2              | 15m       | 98               | 43  | 501               | 53  |
| FA             | 47m       | 22               | 16  | 34                | 18  |
| 3              | 72m       | 153              | 78  | 862               | 124   |
| 4              | 200m      | 149              | 82  | 1337              | 120   |
| 5              | 300m      | 142              | 61  | 1316              | 95  |
| FR             | 393m      | 12               | 2   | 55                | 4   |
| XA             | 434m      | 92               | 41  | 368               | 59  |
| 6              | 579m      | 191              | 115   | 3377              | 189   |
| 7              | 700m      | 157              | 72  | 2168              | 95  |
| TA             | 737m      | 15               | 5   | 35                | 5   |
| FE             | 850m      | 63               | 30  | 181               | 30  |
| 8              | 873m      | 115              | 61  | 1305              | 92  |
| 9              | 927m      | 129              | 82  | 2053              | 150   |
| Total          |           | 294              | 290   | 14026             | 1100  |

### 3.2 Correspondence between species delimited morphologically and by DNA barcoding

Most of species had between two and nine sequences ( $S=226$ ), and ten species had between 10 and 20 sequences (Table 2). Fifty-four species had one sequence each (singletons) (Table 3). The Neighbor Joining phenogram (Appendix 2III), barcode gap analysis (Appendix 3III), and intra and interspecific pairwise distances of the species revealed by DNA barcoding (Appendix 4III) showed that 11 singletons grouped with the 236 species with two or more sequences (Table 4). The remaining singletons could not be analyzed because of the impossibility to determine intraspecific distances, but distances to nearest neighbor are given in Table 3. The mean and maximum intraspecific distance and distance to nearest neighbor of the 236 morphologically delimited species of Arctiinae and the main subordinate taxa with two or more sequences are given in Table 2. Although the mean and maximum intraspecific distances are lower than distance to nearest neighbor in all higher taxa, our results indicated that DNA barcoding and morphology discriminated 161 Arctiinae species equally well, with mean and maximum intraspecific distance of 0.22 and 0.35, respectively and a mean distance to the nearest neighbor of 5.96. From the 161 species, 102 are identified to species, 42 to genus and 17 to tribe/subtribe (see Appendix 1III). DNA

barcode and morphology did not match for 86 entities. The mean and maximum intraspecific distance for those were 2.77 and 4.81, respectively and the mean distance to the nearest neighbor 2.04. Of the 86 entities, 34 were identified to species, 43 to genus and 9 to tribe/subtribe (see Appendix 1III).

**Table 2.** Number of species with two or more sequences, intra and interspecific distances (and standard errors) for Arctiinae and lower taxa.

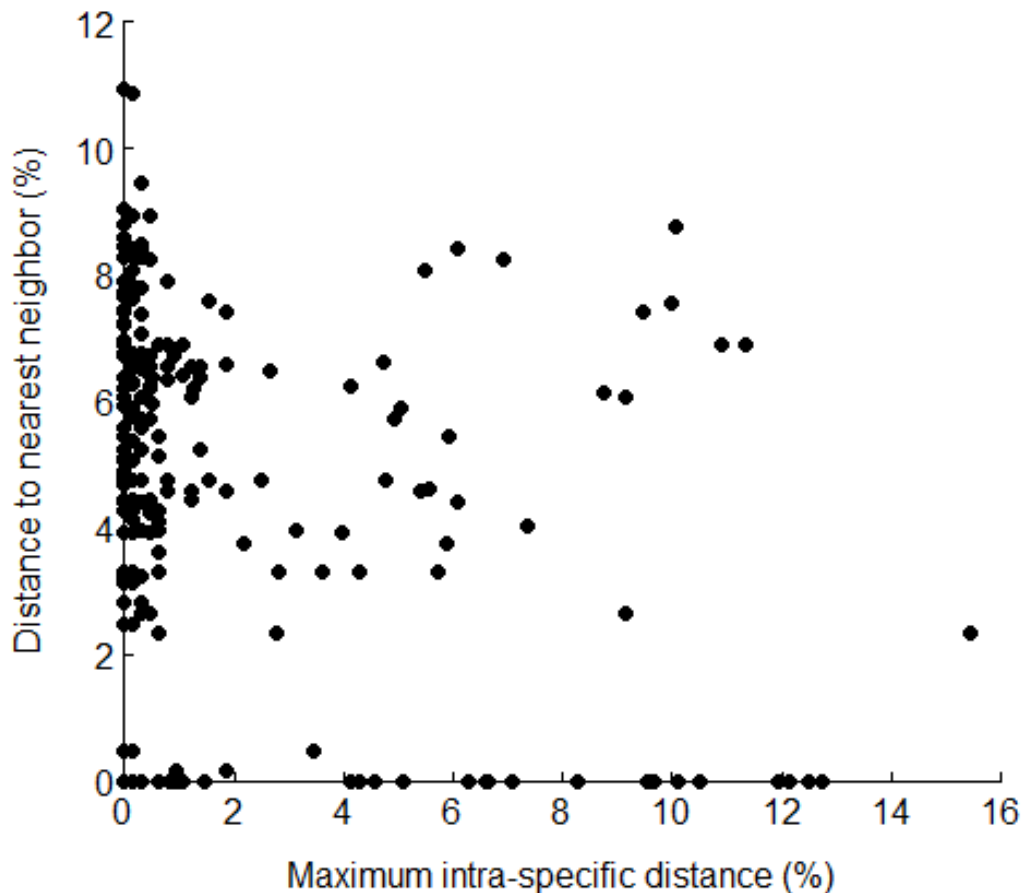
| Taxa          | Number of morphologically delimited species | Number of Sequences | Mean intra-specific distance | Mean Maximum intra-specific distance | Mean distance to nearest neighbor |
|---------------|---|---------------------|------------------------------|--------------------------------------|-----------------------------------|
| Arctiinae     | 236   | 1046                | $1.05 \pm 0.12$              | $1.81 \pm 0.20$                      | $4.70 \pm 0.18$                   |
| Arctiini      | 199   | 856                 | $1.08 \pm 0.14$              | $1.87 \pm 0.23$                      | $4.78 \pm 0.19$                   |
| Arctiina      | 6   | 32                  | $1.43 \pm 0.83$              | $2.52 \pm 1.44$                      | $8.09 \pm 0.45$                   |
| Pericopina    | 10  | 44                  | $1.95 \pm 1.02$              | $2.85 \pm 1.40$                      | $4.95 \pm 0.59$                   |
| Ctenuchina    | 36  | 140                 | $1.00 \pm 0.39$              | $1.49 \pm 0.47$                      | $4.67 \pm 0.50$                   |
| Euchromiina   | 34  | 130                 | $0.59 \pm 0.20$              | $1.87 \pm 0.40$                      | $4.84 \pm 0.32$                   |
| Phaegopterina | 113   | 510                 | $1.16 \pm 0.17$              | $2.12 \pm 0.32$                      | $4.60 \pm 0.27$                   |
| Lithosiini    | 37  | 190                 | $0.88 \pm 0.25$              | $1.45 \pm 0.41$                      | $4.29 \pm 0.49$                   |

**Table 3.** Number of species with one sequence (singletons) and mean distance to nearest neighbor and standard errors for Arctiinae and lower taxa.

| Taxa          | Number of singletons | Mean distance to nearest neighbor |
|---------------|----------------------|-----------------------------------|
| Arctiinae     | 54                   | $5.54 \pm 0.43$                   |
| Arctiini      | 48                   | $5.06 \pm 0.43$                   |
| Arctiina      | 3                    | $2.42 \pm 0.12$                   |
| Pericopina    | 3                    | $7.19 \pm 0.28$                   |
| Ctenuchina    | 14                   | $5.50 \pm 0.78$                   |
| Euchromiina   | 9                    | $6.22 \pm 0.34$                   |
| Phaegopterina | 19                   | $3.63 \pm 0.80$                   |
| Lithosiini    | 6                    | $9.40 \pm 0.68$                   |

Figure 1 shows the maximum intraspecific distance of the species with two or more sequences plotted against distance to the nearest neighbor. This allowed us to verify three kinds of rearrangements in the species identities: 1) clustering, 2) break-up, and 3) break-up and clustering. In the first rearrangement, two or three species clustered together in the same clade (low intraspecific distance and low distance to the nearest neighbor); in the second, individuals of the same species separated in two, three or four clades (high intraspecific distance and high distance to the nearest neighbor); in the third rearrangement one species separated in two clades and one of the clades clustered with a different species (high

intraspecific distance and low distance to the nearest neighbor). Table 4 shows the number of species in each rearrangement category for Arctiinae and the main subordinated taxa (for example see Appendix 1III). DNA barcoding performed better for *Euchromiina* morphospecies than for other taxa (Table 4).



**Figure 1.** Relation between maximum intraspecific distance and distance to nearest neighbor in the morphologically delimited species with two or more sequences. The black dots represent the 236 species.

After the reassessment of external morphology we were able to identify three sources of disagreement that explain the rearrangements in the 86 entities with no correspondence between morphology and DNA barcoding: 1) ineffectiveness of DNA barcoding to separate species clearly delimited by morphology (i.e. changes in COI sequence resulting in paraphyletic and polyphyletic species (Funk and Omland, 2003)); 2) unknown sexual dimorphism; and 3) inaccuracy in delimitation of morphological species (Table 5). We were not able to determine the source of disagreement between external morphology and DNA barcoding for 49 entities, and genitalic morphology of the specimens should be assessed (Table 5). The percentage of species where genitalic morphology should be assessed is

similar in most of lower taxa, except for Arctiina and Lithosiini (Table 5) because the species included in the genera *Paracles* and *Agylla*, respectively. Appendix 1III gives a detailed list of morphological species and the species revealed by DNA barcoding classified according to the different kinds of rearrangements and their sources of disagreement. After the recalculation of pairwise distances in the species revealed by DNA barcoding (Appendix 4III) we found the following intra and interspecific distances for Arctiinae: mean and maximum intraspecific distances of 0.24 and 0.38; mean distance to nearest species 5.62.

**Table 4.** Tally of results of barcoding morphologically defined species of Arctiinae and lower taxa in the Serra da Graciosa, Brazil. We analyzed 236 morphologically defined species with two or more sequences and 11 singletons (see text for details).

| Taxa          | Number of clustering | Number of break up | Number of clustering and break up | Number of morphologically delimited species in accordance with species revealed by DNA barcoding |
|---------------|----------------------|--------------------|-----------------------------------|--|
| Arctiinae     | 40 (16.19%)          | 27 (10.93%)        | 19 (7.69%)                        | 161 (65.19%)   |
| Arctiini      | 32 (15.24%)          | 24 (11.43%)        | 16 (7.62%)                        | 138 (65.71%)   |
| Arctiina      | –                    | 2 (33.33%)         | –                                 | 6 (66.67%)   |
| Pericopina    | 1(11.11%)            | 1 (11.11%)         | –                                 | 7 (77.78%)   |
| Ctenuchina    | 10 (25%)             | 3 (7.5%)           | 4 (10%)                           | 23 (57.5)  |
| Euchromiina   | 1 (2.94%)            | 4 (11.76%)         | –                                 | 29 (85.3%)   |
| Phaegopterina | 20 (16.53%)          | 14 (11.57%)        | 12 (9.92%)                        | 75 (61.98%)  |
| Lithosiini    | 8 (21.62%)           | 3 (8.11%)          | 3 (8.11%)                         | 23 (62.16%)  |

### 3.3 Species richness in the Serra da Graciosa revealed by morphology and DNA barcoding

The number of barcoded Arctiinae species and individuals in the Lepidoptera of Serra do Mar project, and species richness and abundance recorded along the elevational transect in Serra da Graciosa are given in Table 1. The average percentage of barcoded species and individuals recorded in the sampling site are  $48.11\% \pm 13SD$  and  $13.41\% \pm 11.67SD$ , respectively.

Total species richness in the Serra da Graciosa is well represented in our DNA barcode library (290 of 294 species), and we have barcodes for 1/12.751 of the total abundance recorded in our biodiversity study. Total morphology-based species richness ( $S=290$ ) was lower than barcode-based species richness ( $S=309$ ), including singletons. However, it is worth to note that when we have DNA barcodes for 1/12.666 of the total abundance the morphology and DNA barcoding species accumulation curves are equivalent (Figure 2), but a slightly change in this proportion (a final proportion of 1/12.751) is enough

to produce a large difference in the species richness. Therefore, the number of species revealed by DNA barcoding could increase with additional sequences.

**Table 5.** Tally of conflicting results between morphologically delimited species and species revealed by DNA barcoding of Arctiinae and lower taxa in the Serra da Graciosa, Brazil.

| Taxa          | Ineffectiveness of DNA barcoding to discriminate between clearly morphologically delimited species | Number of morphologically delimited species with unknown sexual dimorphism revealed by DNA barcoding | Number of incorrectly morphologically discriminated species revealed by DNA barcoding | Number of species with disagreement between morphology and DNA barcoding delimitations where genitalic morphology should be assessed |
|---------------|--|--|---|--|
| Arctiinae     | 7 (8.14%)  | 16 (18.60%)  | 14 (16.27%)   | 49 (56.97%)  |
| Arctiini      | 7 (9.72%)  | 16 (22.22%)  | 13 (18.05%)   | 36 (50%)   |
| Arctiina      | -  | -  | -   | 2 (100%)   |
| Pericopina    | 1 (50%)  | -  | -   | 1 (50%)  |
| Ctenuchina    | 2 (11.76%)   | 4 (23.52%)   | 2 (11.76%)  | 9 (52.94%)   |
| Euchromiina   | -  | -  | 2 (40%)   | 2 (40%)  |
| Phaegopterina | 4 (8.69%)  | 11 (23.91%)  | 9 (19.56%)  | 22 (47.82%)  |
| Lithosiini    | -  | -  | 1 (7.14%)   | 13 (92.85%)  |

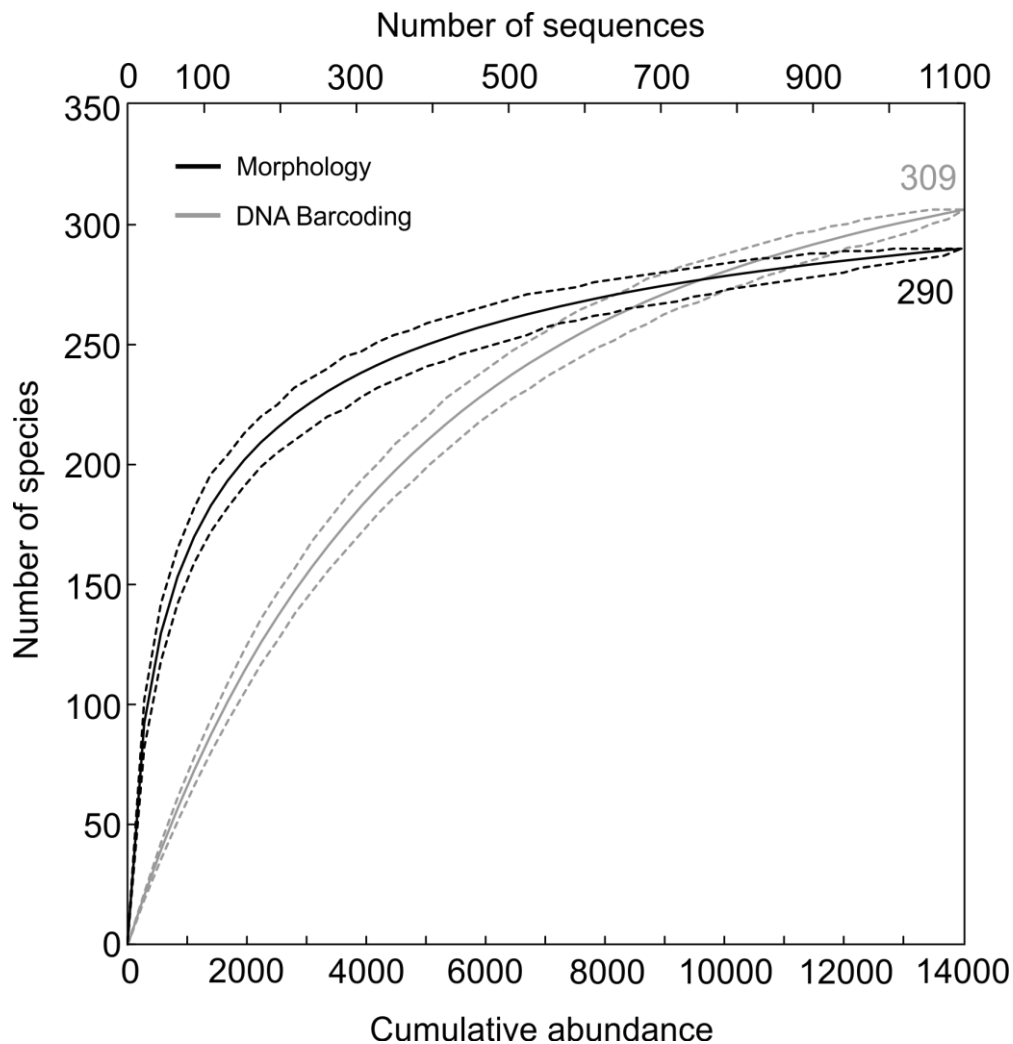
#### 4. Discussion

The effectiveness of DNA barcoding to discriminate species of Lepidoptera has been assessed since the beginning of development of DNA barcoding, with good results in most of times (Hebert, 2003a, b; Hajibabaei et al., 2006; deWard et al., 2011; Hausmann et al., 2011). However, the inventory of the entire caterpillar fauna and their parasitoids of Area de Conservación Guanacaste (ACG) in northwestern Costa Rica (Janzen and Hallwachs, 2005) was the first test to the application of DNA barcoding to complex and species-rich biotas (Janzen et al., 2005). Terrestrial ACG is 115,000 ha of dry forest, rain forest, cloud forest, and their intergrades from 0 to 2000 m a.s.l. (<http://www.acguanacaste.ac.cr>; Janzen 2000). Almost 200,000 caterpillars of 2,810 morphospecies originated from the several habitats within ACG were reared and all life stages documented. In 2003 DNA barcoding was integrated in the inventory and since then the ACG set the standard for the integration of DNA barcoding into Lepidoptera biodiversity studies. One of the clearest outcomes of the ACG study is that the number of specimens for each species must be large (at least 20 specimens). This is because even in a “good” species with four or five individuals in the same cluster and zero intraspecific genetic distance cryptic species can be detected whether more

sequences are added, especially if those specimens originated from different habitats and/or distant located regions (Janzen et al., 2005, 2009). This is in contrast to our results because most of species in our study had between two and nine specimens (sequences) and we have several singletons. Therefore, the species richness revealed by DNA barcoding in our sampling area (309, including singletons) may be an underestimate for the Serra da Graciosa, and there could be an increase in species richness if more sequences were added. Similarly, the number of morphological species could also increase if we had used an integrative taxonomical approach (Schlick-Steiner et al., 2010), but the number of species revealed by DNA barcoding could still be higher, as noted elsewhere (Strutzenberger, et al., 2010). Another important aspect of the ACG inventory was the possibility to correlate barcode clustering with habitat, adult body weight, facies and genitalia morphology, and immature stages morphology. Indeed, the ACG inventory has been ongoing for 50 years and more than 150 members of taxasphere (including 50 professional taxonomists) contributed to its development (Janzen et al, 2005, 2009) while ours is a much smaller size project that employed two taxonomists. Although our results are not directly comparable to those of ACG, some aspects are similar. For instance, DNA barcoding was useful to reveal sexual dimorphism in ACG moths (Janzen et al., 2005) and bees (Sheffield et al., 2009). We found 16 cases of previously unknown sexual dimorphism (Table 5). This information is taxonomically valuable because in many cases specimens of different sexes have been described as separated species (e.g. Mitchell, 1960, 1962). It has also been noted that DNA barcoding is more efficient to distinguish between morphological species when compared to the “human eye”, as in the highly diverse and poorly taxonomically studied geometrid genus *Eois* (Strutzenberger, et al., 2010) or even morphologically well studied butterflies (Dinca et al., 2010). This may be in agreement to our results because the barcoding showed we have incorrectly assigned 14 morphospecies while only seven species were incorrectly assigned by the barcoding (Table 4). However, further morphological studies are needed to determine the source of disagreement in the remaining 50 species (Table 4).

Although our project is far from being an ideal library of DNA barcodes, it is expected to be very useful to ecological studies and the understanding of insect-plant relationship in the Atlantic Forest. Based on our library, immature stages of 102 species where DNA barcoding corresponded to morphology can be reliably identified, and the host-plant could be linked to the adult if a single caterpillar found feeding in a tree is barcoded (see Janzen et al., 2005; Strutzenberger, et al., 2010). Also, the diet analysis of the insectivorous predators can be assessed by barcoding the stomach contents of bats, birds,

small mammals, frogs, lizards and other predators (Valentini, et al., 2009). Indeed, the Bold Systems database has been used successfully to reveal the diet of bats in Canada (Clare et al., 2011). Therefore, we believe that our contribution to the library of barcodes of arctiines will be of great help for the study of food webs and their dynamics in the Atlantic forest in the future.



**Figure 2.** Species accumulation curve based on cumulative abundance and DNA barcode sequences (including singletons). Numbers at the end of the curves are species richness.

Although the effectiveness of DNA barcoding to distinguish between species of Lepidoptera has been confirmed in previously cited works (this effectiveness is between 90% (Dinca et al., 2010) and 98.9% (Hausmann et al., 2011)) some authors suggests a low performance of this method (Whalberg et al., 2003; Elias et al., 2007; Wiemers and Fiedler, 2007; Silva-Brandão et al., 2008). The most frequent argument against the use of barcodes is



interspecific hybridization and the consequent introgression of the mtDNA, as demonstrated by Schmidt and Sperling (2008) in a study of the tiger moth genus *Grammia*. One possible case of introgression in our study is between the sibling species *Phagoptera fusca* and *Pachydota* sp. JAT01. In the first case the mean and maximum intraspecific distance within *P. fusca* is 1.68 and 3.45, respectively but the distance to *Pachydota* sp. JAT01 is 0.46 (see Appendix 3III). Also, the only specimen of *Pachydota* sp. JAT01 clustered with another of *P. fusca* in the Neighbor Joining phenogram (see Appendix 2III). Although this is apparently a case of hybridization, it is not possible to determine precisely whether introgression had occurred without comparing more sequences and/or performing cross-breeding experiments. We prefer not to speculate with regard to the remaining five cases where DNA barcoding was ineffective to distinguish between morphological species (Appendix 4III). Other arguments pointing to the ineffectiveness of DNA barcoding are the amplification of nuclear pseudogenes of the mitochondrial genome or (NUMTs; Song et al., 2008), *Wolbachia* and other parasite infections (Hurst and Jiggins, 2005; Smith et al., 2012), and different rates of genome evolution (Epenbeck et al., 2006). Finally, it has been estimated that 23% of species on earth are paraphyletic or polyphyletic (Funk and Omland, 2003), while barcoding methods assume species monophyly.

The exchange of biodiversity information through the World Wide Web is an important step towards understanding life on earth (Soberón and Peterson, 2004; Godfray et al., 2007; Janzen, 2010). In this context the Barcode of Life Data Systems provides an integrated on-line environment for the assembly and use of DNA barcoding as an auxiliary tool for taxonomy (BOLD Systems, 2012). We believe that as a consequence of the evolution of taxonomy (Scoble, 2004) barcodes will have an important role in new species descriptions in the future (and it does have importance today, see publication at <http://www.barcodinglife.com/>), especially as part of an integrated taxonomic approach. Although it was not our intention to build a comprehensive library of barcodes for Arctiinae our contribution to this goal is substantial. We also tested the integration of DNA barcoding in a biodiversity study of a taxonomically poorly understood and highly diverse group of moths with good results. Future studies will further evaluate the efficiency of the DNA library of barcodes to identify Arctiinae species.

### Acknowledgements

We would like to thank the Brazilian government funding agencies CNPq (Conselho Nacional de Desenvolvimento Científico e Tecnológico, process number 141142/2009-0) and CAPES (Comissão de Aperfeiçoamento de Pessoal de Nível Superior, process number 5708-11-7) for the first author's scholarships. We gratefully acknowledge the University of New Orleans (USA) for the support during the period when the first author visited this institution and to Dr. Michel Laguerre (Institut Européen de Chimie et Biologie, France) for the identification of the *Lithosiini* species, and Dr. Viviane G. Ferro for the collaboration. Finally, we especially thank all the inhabitants of the Serra da Graciosa for the great help during the course of this study.

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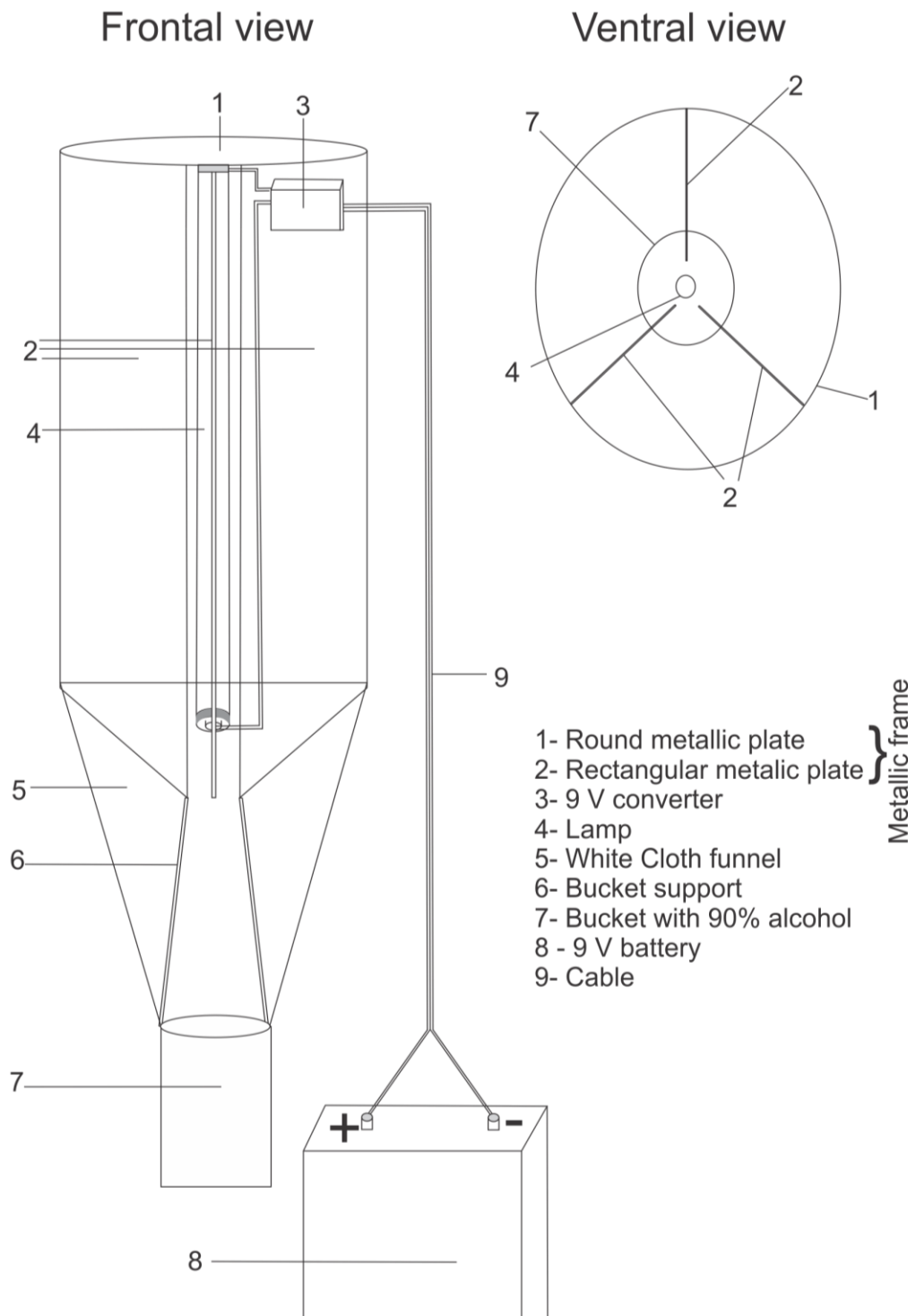
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## Appendix 1I: Trap design details



## Appendix 2I: List of specie with abundance data.

| Species                     | 1  | 2  | FA | 3  | 4  | 5  | FR | XA | 6  | 7  | TA | FE | 8  | 9  | TOTAL |
|-----------------------------|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-------|
| <b>Arctiini</b>             |    |    |    |    |    |    |    |    |    |    |    |    |    |    |       |
| <b>Arctiina</b>             |    |    |    |    |    |    |    |    |    |    |    |    |    |    |       |
| <i>Hypercompe</i>           |    |    |    |    |    |    |    |    |    |    |    |    |    |    |       |
| <i>spJAT01</i>              | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 1  | 0  | 0  | 0  | 11 | 12    |
| <i>Isia alcumena</i>        | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 6  | 6     |
| <i>Paracles fusca</i>       | 5  | 2  | 1  | 2  | 0  | 0  | 0  | 1  | 4  | 2  | 0  | 20 | 4  | 2  | 43    |
| <i>Paracles spJAT01</i>     | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 2  | 0  | 0  | 2     |
| <i>Paracles spJAT02</i>     | 0  | 0  | 0  | 0  | 0  | 1  | 0  | 0  | 0  | 0  | 0  | 1  | 0  | 0  | 2     |
| <i>Paracles spJAT03</i>     | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 1  | 1     |
| <i>Paracles spJAT04</i>     | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 1  | 1     |
| <i>Paracles variegata</i>   | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 2  | 0  | 1  | 3     |
| <i>Virbia divisa</i>        | 11 | 8  | 0  | 15 | 31 | 34 | 4  | 5  | 6  | 2  | 0  | 0  | 0  | 1  | 117   |
| <b>TOTAL</b>                | 16 | 10 | 1  | 17 | 31 | 35 | 4  | 6  | 10 | 5  | 0  | 25 | 4  | 23 | 187   |
| <b>Ctenuchina</b>           |    |    |    |    |    |    |    |    |    |    |    |    |    |    |       |
| <i>Aclytia heber</i>        | 0  | 0  | 1  | 3  | 0  | 1  | 0  | 0  | 2  | 0  | 0  | 0  | 1  | 0  | 8     |
| <i>Aclytia jonesi</i>       | 3  | 0  | 0  | 3  | 0  | 1  | 0  | 2  | 4  | 2  | 0  | 0  | 0  | 1  | 16    |
| <i>Aclytia spJAT01</i>      | 3  | 1  | 0  | 3  | 8  | 12 | 1  | 13 | 68 | 22 | 0  | 0  | 5  | 1  | 137   |
| <i>Aclytia spJAT02</i>      | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 1  | 0  | 0  | 0  | 0  | 0  | 1     |
| <i>Aclytia terra</i>        | 2  | 0  | 0  | 0  | 2  | 1  | 0  | 4  | 9  | 0  | 0  | 1  | 0  | 3  | 22    |
| <i>Agyrta albisparsa</i>    | 6  | 5  | 1  | 3  | 9  | 4  | 0  | 2  | 1  | 9  | 0  | 0  | 2  | 1  | 43    |
| <i>Arctiinae spJAT01</i>    | 1  | 1  | 0  | 2  | 3  | 2  | 0  | 1  | 5  | 0  | 0  | 0  | 0  | 0  | 15    |
| <i>Arctiinae spJAT02</i>    | 0  | 0  | 0  | 2  | 0  | 1  | 0  | 0  | 1  | 1  | 0  | 0  | 0  | 1  | 6     |
| <i>Arctiinae spJAT03</i>    | 0  | 0  | 0  | 0  | 1  | 0  | 0  | 1  | 3  | 0  | 0  | 0  | 0  | 0  | 5     |
| <i>Arctiinae spJAT04</i>    | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 1  | 0  | 0  | 0  | 0  | 0  | 1     |
| <i>Arctiinae spJAT05</i>    | 0  | 0  | 0  | 1  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 1     |
| <i>Arctiinae spJAT06</i>    | 1  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 1  | 2  | 0  | 0  | 0  | 0  | 4     |
| <i>Arctiinae spJAT07</i>    | 1  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 1     |
| <i>Argyrooides</i>          |    |    |    |    |    |    |    |    |    |    |    |    |    |    |       |
| <i>sanguinea</i>            | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 1  | 1     |
| <i>Atypopsis spJAT01</i>    | 0  | 0  | 1  | 0  | 0  | 1  | 2  | 0  | 5  | 1  | 0  | 1  | 0  | 0  | 11    |
| <i>Correbia lycoides</i>    | 0  | 0  | 0  | 0  | 6  | 4  | 0  | 8  | 42 | 8  | 0  | 0  | 2  | 4  | 74    |
| <i>Correbia elegans</i>     | 1  | 3  | 0  | 1  | 2  | 4  | 0  | 2  | 21 | 1  | 0  | 0  | 0  | 1  | 36    |
| <i>Correbia spJAT01</i>     | 0  | 1  | 0  | 1  | 3  | 3  | 0  | 3  | 18 | 3  | 0  | 0  | 0  | 0  | 32    |
| <i>Correbia spJAT02</i>     | 1  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 1     |
| <i>Ctenucha jonesi</i>      | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 1  | 0  | 1     |
| <i>Cyanopepla jucunda</i>   | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 1  | 1  | 0  | 0  | 0  | 1  | 3     |
| <i>Delphyre flaviceps</i>   | 2  | 0  | 0  | 6  | 4  | 2  | 0  | 0  | 2  | 0  | 0  | 0  | 0  | 0  | 16    |
| <i>Delphyre hebes</i>       | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 1  | 0  | 0  | 0  | 0  | 0  | 1     |
| <i>Delphyre pyroperas</i>   | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 1  | 0  | 0  | 0  | 0  | 0  | 1     |
| <i>Delphyre spML01</i>      | 4  | 1  | 0  | 0  | 7  | 10 | 0  | 1  | 9  | 4  | 0  | 1  | 1  | 0  | 38    |
| <i>Demolis albicostata</i>  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 1  | 0  | 0  | 1     |
| <i>Epidesma spJAT01</i>     | 0  | 0  | 1  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 1     |
| <i>Epidesma spJAT02</i>     | 0  | 0  | 1  | 0  | 2  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 3     |
| <i>Epidesma ursula</i>      | 0  | 0  | 0  | 1  | 1  | 0  | 0  | 0  | 1  | 0  | 0  | 0  | 0  | 0  | 3     |
| <i>Episcepsis endodasia</i> | 1  | 0  | 0  | 0  | 0  | 1  | 0  | 0  | 12 | 8  | 0  | 0  | 0  | 0  | 22    |
| <i>Episcepsis venata</i>    | 0  | 1  | 0  | 0  | 3  | 1  | 0  | 1  | 0  | 0  | 0  | 0  | 0  | 0  | 6     |
| <i>Euagra spJAT01</i>       | 0  | 1  | 0  | 0  | 0  | 0  | 0  | 0  | 2  | 0  | 0  | 0  | 0  | 0  | 3     |
| <i>Euagra spJAT02</i>       | 1  | 1  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 2     |
| <i>Eucereon apicalis</i>    | 0  | 0  | 0  | 1  | 2  | 9  | 0  | 15 | 78 | 17 | 2  | 1  | 15 | 19 | 159   |
| <i>Eucereon chalcodon</i>   | 0  | 0  | 0  | 2  | 1  | 0  | 0  | 0  | 3  | 4  | 0  | 0  | 0  | 0  | 10    |
| <i>Eucereon discolor</i>    | 0  | 0  | 0  | 1  | 5  | 4  | 0  | 1  | 16 | 7  | 0  | 0  | 1  | 4  | 39    |
| <i>Eucereon griseata</i>    | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 7  | 8  | 0  | 0  | 1  | 1  | 17    |
| <i>Eucereon quadricolor</i> | 1  | 5  | 1  | 5  | 6  | 18 | 1  | 5  | 18 | 5  | 0  | 0  | 2  | 1  | 68    |
| <i>Eucereon rosa</i>        | 1  | 1  | 0  | 3  | 5  | 5  | 0  | 6  | 4  | 2  | 0  | 0  | 0  | 0  | 27    |
| <i>Eucereon setosum</i>     | 0  | 1  | 0  | 0  | 3  | 4  | 0  | 2  | 2  | 10 | 0  | 0  | 2  | 2  | 26    |
| <i>Eucereon spJAT01</i>     | 16 | 5  | 0  | 5  | 4  | 2  | 0  | 0  | 0  | 0  | 0  | 1  | 0  | 0  | 33    |
| <i>Eucereon spJAT02</i>     | 0  | 0  | 0  | 1  | 3  | 1  | 0  | 1  | 0  | 1  | 0  | 0  | 0  | 0  | 7     |
| <i>Eucereon spJAT03</i>     | 0  | 0  | 0  | 1  | 0  | 1  | 0  | 0  | 1  | 0  | 0  | 0  | 0  | 0  | 3     |
| <i>Eucereon spJAT04</i>     | 0  | 1  | 0  | 1  | 7  | 1  | 0  | 1  | 14 | 0  | 0  | 0  | 0  | 0  | 25    |
| <i>Eucereon spJAT05</i>     | 0  | 0  | 0  | 0  | 1  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 0  | 1     |
| <i>Eucereon tarona</i>      | 0  | 0  | 0  | 1  | 1  | 0  | 0  | 0  | 1  | 1  | 0  | 0  | 0  | 0  | 4     |
| <i>Euceriodes wernickei</i> | 1  | 1  | 1  | 3  | 1  | 2  | 0  | 0  | 10 | 3  | 0  | 0  | 1  | 0  | 23    |
| <i>Galethalea pica</i>      | 0  | 0  | 0  | 0  | 1  | 0  | 0  | 3  | 22 | 7  | 0  | 1  | 14 | 21 | 69    |
| <i>Hyaleucerea</i>          |    |    |    |    |    |    |    |    |    |    |    |    |    |    |       |
| <i>vulnerata</i>            | 0  | 2  | 0  | 2  | 3  | 2  | 0  | 1  | 7  | 1  | 0  | 1  | 0  | 1  | 20    |

|                                |    |    |   |    |     |     |   |    |     |     |   |    |    |     |      |
|--------------------------------|----|----|---|----|-----|-----|---|----|-----|-----|---|----|----|-----|------|
| <i>Napata</i> spJAT01          | 8  | 12 | 0 | 13 | 9   | 7   | 0 | 1  | 10  | 3   | 0 | 0  | 0  | 0   | 63   |
| <i>Philoros affinis</i>        | 2  | 0  | 0 | 9  | 2   | 2   | 0 | 2  | 10  | 1   | 0 | 1  | 2  | 1   | 32   |
| <i>Pseudosphex rubripalpus</i> | 0  | 0  | 0 | 0  | 1   | 0   | 0 | 0  | 9   | 0   | 0 | 0  | 0  | 1   | 11   |
| <i>Sciopsyche tropica</i>      | 0  | 0  | 0 | 1  | 0   | 0   | 0 | 0  | 0   | 0   | 0 | 0  | 0  | 0   | 1    |
| <i>Theages leucophaea</i>      | 0  | 1  | 0 | 1  | 1   | 0   | 0 | 1  | 26  | 0   | 0 | 0  | 0  | 0   | 30   |
| <i>Tipulodes ima</i>           | 0  | 0  | 1 | 0  | 1   | 0   | 0 | 0  | 1   | 0   | 0 | 0  | 0  | 0   | 3    |
| <b>TOTAL</b>                   | 56 | 44 | 8 | 76 | 108 | 106 | 4 | 77 | 450 | 132 | 2 | 9  | 50 | 65  | 1187 |
| <b>Euchromiina</b>             |    |    |   |    |     |     |   |    |     |     |   |    |    |     |      |
| <i>Arctiinae</i> spJAT08       | 0  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 0   | 0   | 0 | 0  | 1  | 0   | 1    |
| <i>Arctiinae</i> spJAT09       | 0  | 0  | 0 | 2  | 1   | 2   | 0 | 0  | 4   | 0   | 0 | 0  | 0  | 0   | 9    |
| <i>Arctiinae</i> spJAT10       | 0  | 0  | 0 | 0  | 0   | 0   | 4 | 0  | 1   | 0   | 0 | 0  | 0  | 0   | 5    |
| <i>Arctiinae</i> spJAT11       | 0  | 1  | 0 | 0  | 0   | 0   | 0 | 0  | 0   | 0   | 0 | 0  | 0  | 0   | 1    |
| <i>Arctiinae</i> spJAT12       | 0  | 0  | 0 | 4  | 0   | 0   | 0 | 0  | 0   | 0   | 0 | 0  | 0  | 0   | 4    |
| <i>Arctiinae</i> spJAT13       | 0  | 0  | 0 | 1  | 0   | 0   | 0 | 0  | 0   | 0   | 0 | 0  | 0  | 0   | 1    |
| <i>Arctiinae</i> spJAT14       | 0  | 0  | 1 | 1  | 0   | 0   | 0 | 0  | 0   | 0   | 0 | 0  | 0  | 0   | 2    |
| <i>Arctiinae</i> spJAT15       | 1  | 0  | 0 | 1  | 1   | 0   | 0 | 0  | 1   | 0   | 0 | 0  | 1  | 0   | 5    |
| <i>Cosmosoma auge</i>          | 0  | 0  | 0 | 1  | 0   | 1   | 0 | 0  | 2   | 0   | 0 | 1  | 1  | 0   | 6    |
| <i>Cosmosoma centrale</i>      | 4  | 0  | 0 | 3  | 4   | 4   | 0 | 1  | 194 | 9   | 1 | 2  | 9  | 18  | 249  |
| <i>Cosmosoma durca</i>         | 1  | 1  | 0 | 2  | 0   | 0   | 0 | 2  | 0   | 6   | 0 | 0  | 2  | 3   | 17   |
| <i>Cosmosoma elegans</i>       | 0  | 0  | 0 | 1  | 5   | 2   | 0 | 0  | 8   | 4   | 0 | 3  | 1  | 8   | 32   |
| <i>Cosmosoma klagesi</i>       | 1  | 0  | 0 | 1  | 2   | 0   | 0 | 0  | 3   | 1   | 0 | 0  | 1  | 0   | 9    |
| <i>Cosmosoma leuconoton</i>    | 0  | 0  | 0 | 2  | 0   | 2   | 0 | 0  | 0   | 0   | 0 | 1  | 0  | 3   | 8    |
| <i>Cosmosoma plutona</i>       | 0  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 0   | 0   | 0 | 2  | 0  | 0   | 2    |
| <i>Cosmosoma</i> spJAT01       | 0  | 0  | 0 | 2  | 1   | 3   | 0 | 3  | 62  | 8   | 0 | 0  | 0  | 1   | 80   |
| <i>Cosmosoma</i> spJAT02       | 0  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 0   | 0   | 0 | 1  | 1  | 1   | 3    |
| <i>Cosmosoma</i> spJAT03       | 0  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 0   | 1   | 0 | 0  | 0  | 0   | 1    |
| <i>Cosmosoma</i> spJAT04       | 1  | 1  | 0 | 1  | 1   | 1   | 0 | 0  | 0   | 0   | 0 | 0  | 0  | 0   | 5    |
| <i>Cosmosoma teuthras</i>      | 1  | 0  | 0 | 2  | 0   | 0   | 0 | 0  | 14  | 0   | 0 | 0  | 0  | 0   | 17   |
| <i>Dinia</i> spJAT01           | 0  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 0   | 0   | 0 | 1  | 0  | 0   | 1    |
| <i>Dycladia lucetius</i>       | 4  | 0  | 0 | 4  | 0   | 0   | 0 | 0  | 0   | 0   | 0 | 0  | 0  | 0   | 8    |
| <i>Erruca cardinalis</i>       | 1  | 0  | 0 | 5  | 5   | 0   | 0 | 0  | 16  | 6   | 0 | 2  | 5  | 34  | 74   |
| <i>Erruca deyrolii</i>         | 3  | 4  | 0 | 2  | 1   | 1   | 0 | 1  | 6   | 2   | 0 | 0  | 0  | 0   | 20   |
| <i>Erruca hanga</i>            | 0  | 0  | 0 | 1  | 3   | 3   | 0 | 1  | 50  | 39  | 0 | 1  | 4  | 31  | 133  |
| <i>Erruca sanguipuncta</i>     | 0  | 0  | 0 | 0  | 0   | 0   | 0 | 1  | 40  | 89  | 0 | 0  | 8  | 19  | 157  |
| <b>Heterodontia</b>            |    |    |   |    |     |     |   |    |     |     |   |    |    |     |      |
| <i>haematica</i>               | 0  | 2  | 1 | 10 | 1   | 0   | 1 | 0  | 0   | 0   | 0 | 0  | 0  | 0   | 15   |
| <i>Holophaea erharda</i>       | 0  | 0  | 0 | 1  | 0   | 0   | 0 | 0  | 1   | 0   | 0 | 0  | 0  | 1   | 3    |
| <b>Ichoria</b>                 |    |    |   |    |     |     |   |    |     |     |   |    |    |     |      |
| <i>chalcomedusa</i>            | 0  | 0  | 0 | 0  | 0   | 2   | 0 | 0  | 2   | 1   | 0 | 0  | 0  | 1   | 6    |
| <i>Ichoria tricineta</i>       | 0  | 0  | 0 | 0  | 1   | 0   | 0 | 1  | 35  | 21  | 0 | 0  | 17 | 31  | 106  |
| <b>Isanthrene</b>              |    |    |   |    |     |     |   |    |     |     |   |    |    |     |      |
| <i>incendiaria</i>             | 0  | 0  | 0 | 0  | 4   | 1   | 0 | 0  | 1   | 1   | 0 | 0  | 0  | 0   | 7    |
| <b>Macrocneme</b>              |    |    |   |    |     |     |   |    |     |     |   |    |    |     |      |
| spJAT01                        | 2  | 0  | 0 | 7  | 0   | 1   | 0 | 1  | 19  | 3   | 0 | 0  | 0  | 0   | 33   |
| <i>Mesothen desperata</i>      | 1  | 2  | 1 | 2  | 0   | 1   | 0 | 1  | 1   | 0   | 0 | 0  | 0  | 0   | 9    |
| <i>Mirandisca harpalyce</i>    | 0  | 0  | 0 | 2  | 1   | 5   | 0 | 1  | 11  | 1   | 0 | 0  | 1  | 2   | 24   |
| <i>Neotrichura nigripes</i>    | 0  | 0  | 0 | 1  | 1   | 0   | 0 | 0  | 3   | 0   | 0 | 0  | 0  | 0   | 5    |
| <i>Nyridela chalciope</i>      | 0  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 2   | 0   | 0 | 0  | 0  | 0   | 2    |
| <b>Phoenicoprocta</b>          |    |    |   |    |     |     |   |    |     |     |   |    |    |     |      |
| <i>haemorrhoidalis</i>         | 0  | 0  | 0 | 2  | 0   | 0   | 0 | 0  | 0   | 0   | 0 | 0  | 0  | 0   | 2    |
| <b>Poliopastea</b>             |    |    |   |    |     |     |   |    |     |     |   |    |    |     |      |
| <i>indistincta</i>             | 0  | 0  | 0 | 2  | 2   | 0   | 0 | 0  | 2   | 0   | 0 | 0  | 1  | 0   | 7    |
| <b>Psilopleura</b>             |    |    |   |    |     |     |   |    |     |     |   |    |    |     |      |
| <i>sanguipuncta</i>            | 6  | 0  | 0 | 23 | 0   | 3   | 0 | 0  | 2   | 0   | 0 | 0  | 1  | 0   | 35   |
| <b>Rhynchopyga</b>             |    |    |   |    |     |     |   |    |     |     |   |    |    |     |      |
| <i>meisteri</i>                | 0  | 0  | 0 | 1  | 0   | 1   | 0 | 0  | 2   | 0   | 0 | 2  | 0  | 3   | 9    |
| <i>Sarosa</i> spML01           | 1  | 0  | 0 | 3  | 0   | 0   | 0 | 0  | 1   | 1   | 0 | 0  | 0  | 1   | 7    |
| <i>Saurita</i> spJAT01         | 0  | 3  | 1 | 5  | 8   | 5   | 0 | 2  | 1   | 0   | 0 | 0  | 0  | 0   | 25   |
| <b>TOTAL</b>                   | 27 | 14 | 4 | 95 | 42  | 38  | 5 | 15 | 484 | 193 | 1 | 16 | 54 | 157 | 1145 |
| <b>Pericopina</b>              |    |    |   |    |     |     |   |    |     |     |   |    |    |     |      |
| <i>Dysschema amphissa</i>      | 2  | 0  | 0 | 9  | 1   | 3   | 0 | 1  | 93  | 54  | 0 | 8  | 9  | 18  | 198  |
| <i>Dysschema fantasma</i>      | 0  | 0  | 0 | 1  | 0   | 0   | 0 | 1  | 20  | 20  | 0 | 0  | 5  | 43  | 90   |
| <i>Dysschema hilarina</i>      | 0  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 0   | 0   | 0 | 1  | 0  | 1   | 2    |
| <i>Dysschema lucifer</i>       | 3  | 0  | 0 | 5  | 2   | 0   | 0 | 0  | 27  | 6   | 0 | 6  | 3  | 19  | 73   |
| <i>Dysschema neda</i>          | 0  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 0   | 0   | 0 | 1  | 0  | 0   | 1    |
| <i>Dysschema sacrificia</i>    | 0  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 0   | 0   | 0 | 0  | 1  | 1   | 2    |
| <i>Dysschema</i> spJAT01       | 0  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 1   | 1   | 0 | 1  | 11 | 27  | 41   |
| <b>Dysschema</b>               |    |    |   |    |     |     |   |    |     |     |   |    |    |     |      |
| <i>subapicalis</i>             | 1  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 0   | 0   | 0 | 0  | 0  | 0   | 1    |
| <i>Episcea extravagans</i>     | 0  | 0  | 0 | 1  | 1   | 0   | 0 | 0  | 1   | 3   | 0 | 0  | 1  | 0   | 7    |
| <i>Euchlaenidia</i>            | 6  | 0  | 0 | 1  | 12  | 12  | 0 | 4  | 12  | 34  | 0 | 0  | 5  | 0   | 86   |

|                              |    |   |   |    |    |    |   |    |     |     |   |    |    |     |     |
|------------------------------|----|---|---|----|----|----|---|----|-----|-----|---|----|----|-----|-----|
| <i>transcisa</i>             |    |   |   |    |    |    |   |    |     |     |   |    |    |     |     |
| <i>Hyalurga fenestrata</i>   | 11 | 5 | 0 | 3  | 15 | 12 | 0 | 11 | 7   | 5   | 1 | 0  | 0  | 0   | 70  |
| <i>Hyalurga</i> spJAT01      | 0  | 1 | 0 | 0  | 1  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 0  | 0   | 2   |
| <i>Sthenognatha gentilis</i> | 0  | 0 | 0 | 0  | 2  | 5  | 0 | 14 | 15  | 17  | 0 | 0  | 0  | 0   | 53  |
| <b>TOTAL</b>                 | 23 | 6 | 0 | 20 | 34 | 32 | 0 | 33 | 176 | 140 | 1 | 17 | 35 | 109 | 626 |
| <b>Phaegopterina</b>         |    |   |   |    |    |    |   |    |     |     |   |    |    |     |     |
| <i>Agaraea semivitre</i>     | 1  | 0 | 1 | 2  | 0  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 0  | 0   | 4   |
| <i>Amalo helops</i>          | 1  | 1 | 0 | 2  | 1  | 3  | 0 | 3  | 4   | 0   | 0 | 0  | 1  | 0   | 16  |
| <i>Amaxia corata</i>         | 4  | 9 | 0 | 4  | 5  | 12 | 0 | 5  | 11  | 4   | 1 | 0  | 2  | 0   | 57  |
| <i>Amaxia hebe</i>           | 3  | 1 | 0 | 4  | 16 | 16 | 0 | 3  | 31  | 23  | 1 | 0  | 7  | 4   | 109 |
| <i>Amaxia</i> spML01         | 0  | 0 | 0 | 0  | 0  | 1  | 0 | 0  | 0   | 0   | 0 | 0  | 0  | 1   | 2   |
| <i>Aphyle abdominalis</i>    | 3  | 0 | 0 | 19 | 0  | 0  | 0 | 0  | 2   | 1   | 0 | 0  | 0  | 0   | 25  |
| <i>Arctiinae</i> spJAT16     | 0  | 0 | 0 | 0  | 1  | 0  | 0 | 1  | 2   | 1   | 0 | 3  | 0  | 5   | 13  |
| <i>Arctiinae</i> spJAT17     | 1  | 0 | 0 | 0  | 0  | 0  | 0 | 0  | 10  | 3   | 0 | 1  | 0  | 0   | 15  |
| <i>Arctiinae</i> spJAT18     | 0  | 0 | 0 | 1  | 1  | 3  | 0 | 0  | 1   | 0   | 0 | 0  | 2  | 2   | 10  |
| <i>Arctiinae</i> spJAT19     | 0  | 2 | 0 | 0  | 0  | 0  | 0 | 1  | 1   | 0   | 0 | 0  | 0  | 0   | 4   |
| <i>Arctiinae</i> spJAT20     | 0  | 0 | 0 | 0  | 0  | 0  | 0 | 0  | 1   | 0   | 0 | 0  | 0  | 0   | 1   |
| <i>Arctiinae</i> spJAT21     | 0  | 0 | 0 | 0  | 0  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 0  | 1   | 1   |
| <i>Arctiinae</i> spJAT22     | 0  | 0 | 0 | 0  | 0  | 0  | 0 | 0  | 1   | 0   | 0 | 0  | 0  | 2   | 3   |
| <i>Arctiinae</i> spJAT23     | 1  | 0 | 0 | 1  | 2  | 2  | 0 | 0  | 0   | 0   | 0 | 1  | 0  | 0   | 7   |
| <i>Arctiinae</i> spJAT24     | 3  | 0 | 0 | 0  | 0  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 0  | 0   | 3   |
| <i>Arctiinae</i> spJAT25     | 0  | 0 | 0 | 0  | 0  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 1  | 0   | 1   |
| <i>Arctiinae</i> spJAT26     | 1  | 0 | 0 | 0  | 2  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 0  | 1   | 4   |
| <i>Arctiinae</i> spJAT27     | 1  | 0 | 0 | 0  | 1  | 1  | 0 | 0  | 0   | 2   | 0 | 0  | 20 | 3   | 28  |
| <i>Arctiinae</i> spJAT28     | 1  | 0 | 0 | 1  | 1  | 1  | 0 | 0  | 0   | 0   | 0 | 0  | 0  | 0   | 4   |
| <i>Arctiinae</i> spJAT29     | 1  | 0 | 0 | 0  | 0  | 0  | 0 | 0  | 0   | 1   | 0 | 0  | 0  | 0   | 2   |
| <i>Arctiinae</i> spJAT30     | 0  | 0 | 0 | 0  | 0  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 1  | 0   | 1   |
| <i>Arctiinae</i> spJAT31     | 0  | 1 | 0 | 0  | 2  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 1  | 1   | 5   |
| <i>Arctiinae</i> spJAT32     | 0  | 0 | 0 | 0  | 0  | 0  | 0 | 0  | 3   | 2   | 0 | 0  | 26 | 0   | 31  |
| <i>Arctiinae</i> spJAT33     | 0  | 1 | 0 | 0  | 0  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 5  | 1   | 7   |
| <i>Arctiinae</i> spJAT34     | 0  | 0 | 0 | 0  | 0  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 6  | 0   | 6   |
| <i>Arctiinae</i> spJAT35     | 0  | 0 | 0 | 0  | 0  | 0  | 0 | 0  | 2   | 0   | 0 | 0  | 0  | 0   | 2   |
| <i>Arctiinae</i> spJAT36     | 0  | 0 | 0 | 0  | 0  | 0  | 0 | 0  | 4   | 7   | 0 | 0  | 8  | 0   | 19  |
| <i>Arctiinae</i> spJAT37     | 0  | 0 | 0 | 0  | 0  | 0  | 0 | 0  | 0   | 1   | 0 | 0  | 2  | 0   | 3   |
| <i>Baritius acuminata</i>    | 0  | 1 | 0 | 2  | 2  | 2  | 0 | 2  | 3   | 2   | 0 | 0  | 0  | 1   | 15  |
| <i>Baritius</i> spML01       | 0  | 7 | 0 | 3  | 5  | 12 | 0 | 16 | 18  | 5   | 0 | 3  | 15 | 6   | 90  |
| <i>Berthonomus piperita</i>  | 0  | 0 | 0 | 0  | 0  | 0  | 0 | 0  | 0   | 1   | 0 | 0  | 4  | 1   | 6   |
| <i>Bertholdia</i>            |    |   |   |    |    |    |   |    |     |     |   |    |    |     |     |
| <i>pseudofumida</i>          | 0  | 0 | 0 | 1  | 0  | 1  | 0 | 1  | 62  | 15  | 0 | 0  | 0  | 1   | 81  |
| <i>Bertholdia soror</i>      | 0  | 0 | 0 | 0  | 0  | 0  | 0 | 0  | 1   | 0   | 0 | 3  | 1  | 12  | 17  |
| <i>Carales astur</i>         | 0  | 0 | 0 | 0  | 3  | 13 | 0 | 0  | 4   | 1   | 0 | 1  | 4  | 1   | 27  |
| <i>Carathis byblis</i>       | 0  | 4 | 0 | 0  | 0  | 1  | 0 | 0  | 1   | 0   | 0 | 0  | 0  | 0   | 6   |
| <i>Castrica</i>              |    |   |   |    |    |    |   |    |     |     |   |    |    |     |     |
| <i>phalaenoides</i>          | 2  | 4 | 0 | 5  | 3  | 3  | 0 | 4  | 3   | 1   | 0 | 0  | 0  | 0   | 25  |
| <i>Cissura decora</i>        | 6  | 2 | 0 | 9  | 13 | 4  | 0 | 0  | 47  | 12  | 1 | 7  | 9  | 39  | 149 |
| <i>Cratoplastis</i>          |    |   |   |    |    |    |   |    |     |     |   |    |    |     |     |
| <i>catherinae</i>            | 0  | 0 | 0 | 5  | 1  | 0  | 0 | 0  | 5   | 5   | 0 | 0  | 0  | 1   | 17  |
| <i>Echeta divisa</i>         | 0  | 0 | 0 | 0  | 0  | 0  | 0 | 0  | 2   | 3   | 0 | 1  | 1  | 3   | 10  |
| <i>Echeta</i> spJAT01        | 0  | 0 | 0 | 0  | 13 | 0  | 0 | 5  | 1   | 0   | 0 | 0  | 0  | 3   | 22  |
| <i>Elysus cingulata</i>      | 0  | 0 | 0 | 0  | 1  | 0  | 0 | 0  | 0   | 1   | 0 | 0  | 0  | 0   | 2   |
| <i>Elysus pyrosticta</i>     | 0  | 2 | 0 | 3  | 0  | 0  | 0 | 0  | 4   | 1   | 0 | 1  | 0  | 0   | 11  |
| <i>Elysus superba</i>        | 0  | 0 | 0 | 0  | 0  | 0  | 0 | 0  | 2   | 1   | 0 | 0  | 0  | 0   | 3   |
| <i>Eupseudosoma</i>          |    |   |   |    |    |    |   |    |     |     |   |    |    |     |     |
| <i>involuta</i>              | 2  | 0 | 0 | 0  | 2  | 0  | 0 | 1  | 2   | 1   | 0 | 0  | 0  | 0   | 8   |
| <i>Graphea</i>               |    |   |   |    |    |    |   |    |     |     |   |    |    |     |     |
| <i>paramarmorea</i>          | 0  | 0 | 0 | 0  | 0  | 1  | 0 | 1  | 0   | 0   | 0 | 0  | 0  | 0   | 2   |
| <i>Haemanota bicolor</i>     | 0  | 0 | 0 | 0  | 5  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 0  | 0   | 5   |
| <i>Hyperandra</i>            |    |   |   |    |    |    |   |    |     |     |   |    |    |     |     |
| <i>appendiculata</i>         | 2  | 0 | 0 | 8  | 0  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 0  | 0   | 10  |
| <i>Hypidalia enervis</i>     | 0  | 0 | 0 | 0  | 0  | 0  | 0 | 0  | 1   | 1   | 0 | 2  | 6  | 9   | 19  |
| <i>Idalus agastus</i>        | 1  | 1 | 0 | 5  | 7  | 2  | 0 | 1  | 8   | 4   | 0 | 1  | 0  | 3   | 33  |
| <i>Idalus lineosus</i>       | 0  | 0 | 0 | 3  | 3  | 1  | 0 | 4  | 21  | 16  | 0 | 1  | 1  | 6   | 56  |
| <i>Idalus</i> spJAT01        | 1  | 2 | 0 | 5  | 17 | 2  | 0 | 3  | 14  | 9   | 0 | 0  | 0  | 0   | 53  |
| <i>Ischnocampa</i>           |    |   |   |    |    |    |   |    |     |     |   |    |    |     |     |
| <i>lugubris</i>              | 0  | 0 | 0 | 1  | 4  | 16 | 0 | 2  | 27  | 10  | 0 | 0  | 22 | 5   | 87  |
| <i>Ischnog0tha</i>           |    |   |   |    |    |    |   |    |     |     |   |    |    |     |     |
| <i>leucapera</i>             | 0  | 0 | 0 | 0  | 0  | 0  | 0 | 0  | 13  | 1   | 0 | 0  | 0  | 1   | 15  |
| <i>Lepidokirbya vittipes</i> | 1  | 1 | 0 | 4  | 5  | 1  | 0 | 2  | 6   | 0   | 0 | 0  | 0  | 0   | 20  |
| <i>Lepidozikania</i>         |    |   |   |    |    |    |   |    |     |     |   |    |    |     |     |
| spJAT01                      | 0  | 0 | 0 | 0  | 1  | 0  | 0 | 0  | 2   | 1   | 0 | 0  | 12 | 15  | 31  |
| <i>Leucanopsis coniota</i>   | 0  | 0 | 0 | 1  | 0  | 0  | 0 | 0  | 0   | 0   | 0 | 0  | 0  | 0   | 1   |
| <i>Leucanopsis leucania</i>  | 0  | 1 | 0 | 1  | 0  | 0  | 0 | 0  | 0   | 1   | 0 | 0  | 0  | 1   | 4   |
| <i>Leucanopsis mandus</i>    | 0  | 0 | 0 | 0  | 0  | 0  | 0 | 0  | 1   | 1   | 0 | 0  | 15 | 7   | 24  |
| <i>Leucanopsis oruba</i>     | 0  | 0 | 0 | 1  | 0  | 1  | 0 | 0  | 4   | 2   | 0 | 2  | 7  | 2   | 19  |

|                             |    |    |   |    |     |     |    |    |     |     |   |   |    |    |     |  |
|-----------------------------|----|----|---|----|-----|-----|----|----|-----|-----|---|---|----|----|-----|--|
| <i>Leucanopsis</i>          |    |    |   |    |     |     |    |    |     |     |   |   |    |    |     |  |
| spJAT01                     | 0  | 0  | 0 | 0  | 1   | 0   | 0  | 0  | 0   | 0   | 0 | 0 | 10 | 0  | 11  |  |
| <i>Leucanopsis</i>          |    |    |   |    |     |     |    |    |     |     |   |   |    |    |     |  |
| spJAT02                     | 0  | 0  | 0 | 0  | 0   | 0   | 0  | 0  | 0   | 0   | 0 | 0 | 3  | 6  | 9   |  |
| <i>Leucanopsis</i>          |    |    |   |    |     |     |    |    |     |     |   |   |    |    |     |  |
| spJAT03                     | 1  | 0  | 0 | 0  | 0   | 1   | 0  | 0  | 1   | 1   | 0 | 0 | 0  | 2  | 6   |  |
| <i>Leucanopsis</i>          |    |    |   |    |     |     |    |    |     |     |   |   |    |    |     |  |
| spJAT04                     | 2  | 0  | 1 | 0  | 1   | 3   | 0  | 0  | 1   | 2   | 0 | 1 | 4  | 0  | 15  |  |
| <i>Leucanopsis</i>          |    |    |   |    |     |     |    |    |     |     |   |   |    |    |     |  |
| spJAT05                     | 0  | 0  | 0 | 0  | 0   | 0   | 0  | 0  | 1   | 0   | 0 | 1 | 3  | 2  | 7   |  |
| <i>Leucanopsis</i>          |    |    |   |    |     |     |    |    |     |     |   |   |    |    |     |  |
| spJAT06                     | 0  | 0  | 0 | 0  | 0   | 0   | 0  | 0  | 0   | 0   | 0 | 0 | 0  | 2  | 2   |  |
| <i>Leucanopsis</i>          |    |    |   |    |     |     |    |    |     |     |   |   |    |    |     |  |
| spJAT07                     | 0  | 0  | 0 | 0  | 0   | 0   | 0  | 0  | 0   | 0   | 0 | 0 | 0  | 4  | 4   |  |
| <i>Leucanopsis</i>          |    |    |   |    |     |     |    |    |     |     |   |   |    |    |     |  |
| spJAT08                     | 0  | 0  | 0 | 0  | 0   | 1   | 0  | 0  | 0   | 0   | 0 | 0 | 1  | 0  | 2   |  |
| <i>Lophocampa arpi</i>      | 0  | 0  | 0 | 0  | 0   | 0   | 0  | 0  | 1   | 1   | 0 | 0 | 0  | 0  | 2   |  |
| <i>Lophocampa</i>           |    |    |   |    |     |     |    |    |     |     |   |   |    |    |     |  |
| spJAT01                     | 0  | 1  | 0 | 0  | 1   | 3   | 0  | 2  | 9   | 14  | 1 | 0 | 11 | 1  | 43  |  |
| <i>Lophocampa</i>           |    |    |   |    |     |     |    |    |     |     |   |   |    |    |     |  |
| spJAT02                     | 0  | 0  | 0 | 3  | 0   | 1   | 0  | 0  | 1   | 0   | 0 | 0 | 0  | 0  | 5   |  |
| <i>Lophocampa texta</i>     | 2  | 1  | 0 | 1  | 1   | 0   | 0  | 0  | 0   | 0   | 1 | 1 | 0  | 2  | 9   |  |
| <i>Machadoia</i>            |    |    |   |    |     |     |    |    |     |     |   |   |    |    |     |  |
| xanthosticta                | 0  | 0  | 0 | 1  | 0   | 2   | 0  | 0  | 2   | 4   | 1 | 0 | 3  | 4  | 17  |  |
| <i>Mazaeras francki</i>     | 4  | 1  | 0 | 3  | 1   | 0   | 0  | 0  | 3   | 1   | 0 | 0 | 0  | 1  | 14  |  |
| <i>Melese castrena</i>      | 22 | 14 | 1 | 16 | 4   | 6   | 1  | 1  | 3   | 22  | 1 | 1 | 23 | 14 | 129 |  |
| <i>Melese chozeba</i>       | 1  | 0  | 0 | 3  | 8   | 30  | 0  | 7  | 104 | 53  | 0 | 3 | 41 | 79 | 329 |  |
| <i>Melese incertus</i>      | 0  | 1  | 0 | 4  | 0   | 0   | 0  | 2  | 0   | 0   | 0 | 0 | 0  | 0  | 7   |  |
| <i>Melese</i> spJAT01       | 16 | 66 | 0 | 36 | 165 | 265 | 3  | 48 | 28  | 9   | 0 | 0 | 3  | 0  | 639 |  |
| <i>Melese</i> spJAT02       | 3  | 9  | 0 | 4  | 0   | 2   | 25 | 1  | 42  | 2   | 0 | 0 | 0  | 1  | 89  |  |
| <i>Melese</i> spJAT03       | 2  | 3  | 0 | 7  | 1   | 2   | 0  | 1  | 1   | 1   | 0 | 0 | 2  | 0  | 20  |  |
| <i>Melese</i> spJAT04       | 6  | 1  | 3 | 16 | 1   | 0   | 0  | 0  | 0   | 0   | 0 | 0 | 0  | 0  | 27  |  |
| <i>Melese</i> spJAT05       | 5  | 2  | 1 | 22 | 15  | 19  | 0  | 3  | 20  | 6   | 0 | 0 | 0  | 1  | 94  |  |
| <i>Melese</i> spJAT06       | 8  | 35 | 0 | 4  | 28  | 8   | 0  | 5  | 6   | 0   | 0 | 0 | 0  | 0  | 94  |  |
| <i>Melese</i> spJAT07       | 10 | 17 | 0 | 13 | 58  | 55  | 0  | 19 | 5   | 2   | 0 | 1 | 1  | 0  | 181 |  |
| <i>Melese</i> spJAT08       | 3  | 2  | 0 | 1  | 2   | 0   | 0  | 0  | 0   | 0   | 0 | 0 | 0  | 0  | 8   |  |
| <i>Melese</i> spJAT09       | 0  | 3  | 0 | 0  | 4   | 8   | 0  | 0  | 4   | 6   | 0 | 0 | 5  | 3  | 33  |  |
| <i>Melese</i> spJAT10       | 2  | 0  | 0 | 3  | 3   | 2   | 0  | 0  | 2   | 0   | 0 | 0 | 1  | 0  | 13  |  |
| <i>Melese</i> spJAT11       | 0  | 0  | 0 | 1  | 0   | 0   | 0  | 0  | 0   | 0   | 0 | 0 | 0  | 0  | 1   |  |
| <i>Melese</i> spJAT12       | 0  | 0  | 0 | 2  | 0   | 1   | 0  | 0  | 0   | 0   | 0 | 0 | 0  | 0  | 3   |  |
| <i>Neidalia dulcicula</i>   | 0  | 0  | 0 | 0  | 0   | 0   | 0  | 0  | 1   | 0   | 0 | 0 | 0  | 0  | 1   |  |
| <i>Neonerita</i>            |    |    |   |    |     |     |    |    |     |     |   |   |    |    |     |  |
| dorsipuncta                 | 0  | 0  | 0 | 0  | 2   | 12  | 0  | 6  | 9   | 1   | 0 | 0 | 0  | 0  | 30  |  |
| <i>Ochrodota</i>            |    |    |   |    |     |     |    |    |     |     |   |   |    |    |     |  |
| pronapides                  | 6  | 9  | 0 | 18 | 25  | 36  | 2  | 3  | 0   | 0   | 0 | 0 | 1  | 0  | 100 |  |
| <i>Opharus basalis</i>      | 0  | 0  | 0 | 0  | 1   | 2   | 0  | 0  | 0   | 1   | 0 | 0 | 1  | 0  | 5   |  |
| <i>Opharus brasiliensis</i> | 0  | 0  | 0 | 0  | 2   | 3   | 0  | 2  | 9   | 1   | 0 | 0 | 0  | 0  | 17  |  |
| <i>Opharus notata</i>       | 0  | 0  | 0 | 0  | 0   | 1   | 0  | 0  | 4   | 10  | 0 | 0 | 11 | 3  | 29  |  |
| <i>Opharus procroides</i>   | 0  | 0  | 0 | 0  | 6   | 23  | 0  | 2  | 27  | 26  | 0 | 0 | 5  | 5  | 94  |  |
| <i>Opharus rema</i>         | 1  | 0  | 0 | 0  | 5   | 1   | 0  | 0  | 12  | 5   | 1 | 0 | 13 | 0  | 38  |  |
| <i>Ormetica iheringi</i>    | 1  | 0  | 0 | 1  | 0   | 0   | 0  | 0  | 10  | 3   | 0 | 0 | 0  | 1  | 16  |  |
| <i>Ormetica rothschildi</i> | 0  | 0  | 0 | 2  | 1   | 1   | 0  | 2  | 32  | 2   | 0 | 0 | 0  | 0  | 40  |  |
| <i>Pachydota affinis</i>    | 0  | 1  | 0 | 1  | 0   | 0   | 0  | 0  | 8   | 1   | 0 | 0 | 0  | 1  | 12  |  |
| <i>Pachydota</i> spJAT01    | 1  | 0  | 0 | 1  | 0   | 0   | 0  | 0  | 1   | 0   | 0 | 0 | 0  | 0  | 3   |  |
| <i>Pareuchaetes</i>         |    |    |   |    |     |     |    |    |     |     |   |   |    |    |     |  |
| spML01                      | 6  | 2  | 0 | 3  | 0   | 2   | 0  | 0  | 0   | 3   | 0 | 0 | 0  | 0  | 16  |  |
| <i>Pelochyta cinerea</i>    | 0  | 1  | 0 | 0  | 3   | 7   | 0  | 3  | 3   | 18  | 0 | 0 | 12 | 1  | 48  |  |
| <i>Pelochyta</i> spJAT01    | 1  | 0  | 0 | 0  | 1   | 1   | 0  | 0  | 0   | 0   | 0 | 0 | 0  | 0  | 3   |  |
| <i>Phaegoptera chorima</i>  | 1  | 0  | 0 | 0  | 0   | 0   | 0  | 0  | 2   | 9   | 0 | 0 | 1  | 4  | 17  |  |
| <i>Phaegoptera fusca</i>    | 0  | 0  | 0 | 0  | 0   | 1   | 0  | 0  | 13  | 28  | 0 | 5 | 59 | 38 | 144 |  |
| <i>Phaegoptera</i>          |    |    |   |    |     |     |    |    |     |     |   |   |    |    |     |  |
| histrionica                 | 0  | 1  | 0 | 0  | 2   | 11  | 0  | 0  | 7   | 43  | 0 | 1 | 11 | 8  | 84  |  |
| <i>Psychophasma erosa</i>   | 0  | 0  | 0 | 0  | 0   | 0   | 0  | 1  | 0   | 2   | 0 | 0 | 0  | 0  | 3   |  |
| <i>Rhipha flavithorax</i>   | 0  | 0  | 0 | 2  | 0   | 0   | 0  | 0  | 1   | 0   | 0 | 0 | 0  | 0  | 3   |  |
| <i>Rhipha subflammanis</i>  | 1  | 0  | 0 | 0  | 0   | 6   | 0  | 0  | 12  | 21  | 0 | 0 | 4  | 2  | 46  |  |
| <i>Robinsonia spitzi</i>    | 0  | 1  | 0 | 0  | 0   | 1   | 0  | 4  | 25  | 25  | 0 | 0 | 16 | 11 | 83  |  |
| <i>Romualdia elongata</i>   | 0  | 0  | 0 | 0  | 0   | 0   | 0  | 0  | 0   | 1   | 0 | 4 | 0  | 0  | 5   |  |
| <i>Scaptius</i> spML01      | 4  | 7  | 0 | 0  | 8   | 3   | 0  | 0  | 1   | 1   | 0 | 0 | 1  | 1  | 26  |  |
| <i>Selenarctia elissa</i>   | 0  | 0  | 0 | 0  | 1   | 0   | 0  | 0  | 3   | 0   | 0 | 0 | 0  | 0  | 4   |  |
| <i>Sutunocrea reducta</i>   | 1  | 0  | 0 | 0  | 1   | 0   | 0  | 1  | 8   | 1   | 0 | 0 | 0  | 0  | 12  |  |
| <i>Sychesia dryas</i>       | 0  | 1  | 0 | 2  | 0   | 3   | 0  | 0  | 4   | 13  | 0 | 0 | 7  | 0  | 30  |  |
| <i>Symphlebia distincta</i> | 3  | 32 | 0 | 2  | 16  | 14  | 0  | 0  | 6   | 12  | 0 | 2 | 2  | 4  | 93  |  |
| <i>Symphlebia</i>           |    |    |   |    |     |     |    |    |     |     |   |   |    |    |     |  |
| lophocampoides              | 0  | 4  | 0 | 3  | 1   | 0   | 0  | 0  | 0   | 1   | 0 | 3 | 1  | 3  | 16  |  |
| <i>Symphlebia perflua</i>   | 6  | 25 | 0 | 23 | 58  | 68  | 0  | 6  | 74  | 158 | 2 | 2 | 78 | 27 | 527 |  |

|                            |     |     |    |     |      |      |    |     |      |      |    |     |      |      |       |
|----------------------------|-----|-----|----|-----|------|------|----|-----|------|------|----|-----|------|------|-------|
| <i>Symphlebia</i> spJAT01  | 0   | 3   | 0  | 0   | 0    | 0    | 0  | 0   | 0    | 0    | 0  | 0   | 0    | 0    | 3     |
| <i>Thysanopygma</i>        |     |     |    |     |      |      |    |     |      |      |    |     |      |      |       |
| <i>pyrropyga</i>           | 0   | 1   | 0  | 1   | 2    | 3    | 0  | 1   | 2    | 1    | 0  | 0   | 0    | 0    | 11    |
| <i>Trichromia</i> spJAT01  | 8   | 21  | 3  | 2   | 17   | 42   | 0  | 6   | 4    | 21   | 0  | 0   | 14   | 4    | 142   |
| <i>Trichromia</i> spJAT02  | 9   | 5   | 0  | 1   | 3    | 5    | 0  | 10  | 3    | 7    | 0  | 0   | 10   | 3    | 56    |
| <i>Trichromia</i> spJAT03  | 1   | 0   | 0  | 1   | 0    | 0    | 0  | 0   | 4    | 4    | 0  | 0   | 3    | 1    | 14    |
| <i>Trichromia</i> spJAT04  | 4   | 2   | 0  | 0   | 6    | 3    | 0  | 0   | 6    | 1    | 0  | 0   | 0    | 0    | 22    |
| <i>Trichromia</i> spJAT05  | 14  | 12  | 0  | 11  | 15   | 20   | 0  | 0   | 8    | 8    | 0  | 0   | 0    | 1    | 89    |
| <i>Trichromia</i> spJAT06  | 11  | 44  | 0  | 7   | 7    | 2    | 0  | 0   | 0    | 0    | 0  | 0   | 0    | 0    | 71    |
| <i>Tricypha imperialis</i> | 0   | 0   | 0  | 0   | 3    | 7    | 0  | 1   | 0    | 3    | 0  | 0   | 2    | 1    | 17    |
| <i>Tricypha</i> spJAT01    | 0   | 1   | 0  | 0   | 1    | 0    | 0  | 1   | 0    | 0    | 0  | 0   | 0    | 0    | 3     |
| <i>Viviennea dolens</i>    | 0   | 0   | 0  | 0   | 0    | 0    | 0  | 0   | 5    | 1    | 0  | 1   | 0    | 0    | 7     |
| <i>Viviennea moma</i>      | 1   | 0   | 0  | 1   | 0    | 0    | 0  | 0   | 4    | 0    | 0  | 0   | 0    | 0    | 6     |
| <i>Viviennea superba</i>   | 0   | 0   | 0  | 0   | 0    | 0    | 0  | 0   | 1    | 0    | 0  | 0   | 0    | 0    | 1     |
| <i>Xanthophaeina levis</i> | 0   | 0   | 0  | 0   | 0    | 1    | 0  | 0   | 10   | 16   | 0  | 1   | 4    | 7    | 39    |
| <b>TOTAL</b>               | 203 | 369 | 10 | 313 | 598  | 787  | 31 | 193 | 878  | 712  | 10 | 54  | 546  | 386  | 5144  |
| <b>Lithosiini</b>          |     |     |    |     |      |      |    |     |      |      |    |     |      |      |       |
| <i>Agylla polysemata</i>   | 5   | 1   | 0  | 3   | 23   | 21   | 0  | 3   | 112  | 90   | 13 | 8   | 120  | 224  | 623   |
| <i>Agylla</i> spJAT01      | 13  | 4   | 2  | 60  | 127  | 35   | 0  | 4   | 565  | 379  | 0  | 1   | 42   | 124  | 1356  |
| <i>Agylla</i> spJAT02      | 25  | 10  | 0  | 74  | 70   | 56   | 0  | 4   | 192  | 340  | 0  | 11  | 184  | 325  | 1291  |
| <i>Agylla</i> spJAT03      | 16  | 6   | 0  | 38  | 30   | 27   | 6  | 18  | 213  | 75   | 7  | 32  | 191  | 475  | 1134  |
| <i>Agylla</i> spJAT04      | 0   | 0   | 4  | 0   | 0    | 0    | 0  | 0   | 0    | 1    | 0  | 1   | 2    | 3    | 11    |
| <i>Agylla</i> spJAT05      | 0   | 0   | 0  | 0   | 0    | 0    | 0  | 0   | 0    | 0    | 0  | 0   | 4    | 0    | 4     |
| <i>Agylla</i> spJAT06      | 0   | 0   | 0  | 0   | 0    | 0    | 0  | 0   | 1    | 8    | 0  | 0   | 1    | 5    | 15    |
| <i>Agylla</i> spJAT07      | 1   | 1   | 0  | 4   | 19   | 1    | 0  | 0   | 8    | 0    | 0  | 0   | 1    | 1    | 36    |
| <i>Agylla</i> spJAT08      | 7   | 1   | 0  | 20  | 94   | 23   | 0  | 0   | 49   | 15   | 0  | 0   | 16   | 23   | 248   |
| <i>Agylla</i> spJAT09      | 7   | 2   | 0  | 32  | 97   | 79   | 5  | 11  | 157  | 45   | 0  | 5   | 19   | 79   | 538   |
| <i>Agylla</i> spJAT10      | 0   | 0   | 0  | 0   | 2    | 2    | 0  | 0   | 0    | 4    | 1  | 0   | 7    | 6    | 22    |
| <i>Agylla</i> spJAT11      | 0   | 0   | 0  | 0   | 0    | 1    | 0  | 0   | 0    | 0    | 0  | 0   | 0    | 1    | 2     |
| <i>Agylla</i> spJAT12      | 7   | 4   | 0  | 19  | 6    | 3    | 0  | 0   | 1    | 1    | 0  | 0   | 0    | 2    | 43    |
| <i>Agylla</i> spJAT13      | 0   | 0   | 0  | 0   | 2    | 2    | 0  | 0   | 1    | 0    | 0  | 0   | 2    | 0    | 7     |
| <i>Agylla</i> spJAT14      | 0   | 0   | 0  | 0   | 0    | 0    | 0  | 0   | 0    | 1    | 0  | 0   | 2    | 0    | 3     |
| <i>Agylla</i> spJAT15      | 0   | 0   | 0  | 0   | 0    | 0    | 0  | 0   | 0    | 2    | 0  | 0   | 21   | 29   | 52    |
| <i>Agylla</i> spML16       | 1   | 0   | 0  | 1   | 9    | 11   | 0  | 0   | 2    | 1    | 0  | 0   | 1    | 5    | 31    |
| <i>Agylla</i> spML17       | 1   | 0   | 0  | 5   | 4    | 0    | 0  | 0   | 7    | 2    | 0  | 0   | 0    | 1    | 20    |
| <i>Apistosis judas</i>     | 0   | 0   | 0  | 1   | 0    | 0    | 0  | 0   | 0    | 0    | 0  | 0   | 0    | 0    | 1     |
| <i>Arctiinae</i> spML38    | 0   | 2   | 0  | 1   | 2    | 2    | 0  | 0   | 2    | 0    | 0  | 0   | 0    | 0    | 9     |
| <i>Arctiinae</i> spJAT39   | 3   | 2   | 0  | 2   | 2    | 1    | 0  | 2   | 10   | 4    | 0  | 1   | 1    | 2    | 30    |
| <i>Arhabdosia</i> spML01   | 0   | 0   | 0  | 0   | 0    | 0    | 0  | 0   | 2    | 0    | 0  | 0   | 0    | 4    | 6     |
| <i>Clemensia</i>           |     |     |    |     |      |      |    |     |      |      |    |     |      |      |       |
| <i>marmorata</i>           | 0   | 0   | 0  | 3   | 0    | 0    | 0  | 0   | 0    | 1    | 0  | 0   | 0    | 0    | 4     |
| <i>Cloesia</i> spML01      | 0   | 3   | 5  | 11  | 7    | 4    | 0  | 0   | 9    | 1    | 0  | 0   | 0    | 0    | 40    |
| <i>Euthyone purpurea</i>   | 0   | 0   | 0  | 0   | 0    | 0    | 0  | 0   | 0    | 0    | 0  | 0   | 0    | 1    | 1     |
| <i>Hypermaepha</i>         |     |     |    |     |      |      |    |     |      |      |    |     |      |      |       |
| spML01                     | 7   | 5   | 0  | 9   | 4    | 7    | 0  | 1   | 0    | 0    | 0  | 0   | 1    | 0    | 34    |
| <i>Illice brunnea</i>      | 1   | 0   | 0  | 6   | 0    | 0    | 0  | 0   | 4    | 1    | 0  | 0   | 0    | 0    | 12    |
| <i>Illice cryptopygra</i>  | 0   | 0   | 0  | 1   | 2    | 0    | 0  | 0   | 0    | 0    | 0  | 0   | 0    | 0    | 3     |
| <i>Illice ditrigona</i>    | 0   | 0   | 0  | 1   | 1    | 9    | 0  | 1   | 25   | 7    | 0  | 0   | 1    | 1    | 46    |
| <i>Illice endoxantha</i>   | 0   | 2   | 0  | 4   | 2    | 13   | 0  | 0   | 0    | 0    | 0  | 0   | 0    | 0    | 21    |
| <i>Illice</i> spML01       | 0   | 0   | 0  | 6   | 0    | 0    | 0  | 0   | 3    | 1    | 0  | 0   | 0    | 0    | 10    |
| <i>Illice</i> spML02       | 0   | 0   | 0  | 1   | 0    | 0    | 0  | 0   | 0    | 0    | 0  | 0   | 0    | 0    | 1     |
| <i>Illice</i> spML03       | 0   | 0   | 0  | 0   | 0    | 2    | 0  | 0   | 2    | 0    | 0  | 0   | 0    | 0    | 4     |
| <i>Illice</i> spML04       | 0   | 0   | 0  | 2   | 0    | 0    | 0  | 0   | 0    | 0    | 0  | 0   | 0    | 0    | 2     |
| <i>Lycomorphodes</i>       |     |     |    |     |      |      |    |     |      |      |    |     |      |      |       |
| spML01                     | 1   | 0   | 0  | 0   | 0    | 2    | 0  | 0   | 0    | 0    | 0  | 0   | 0    | 0    | 3     |
| <i>Lycomorphodes</i>       |     |     |    |     |      |      |    |     |      |      |    |     |      |      |       |
| <i>strigosa</i>            | 0   | 2   | 0  | 2   | 0    | 1    | 0  | 0   | 0    | 0    | 0  | 0   | 0    | 0    | 5     |
| <i>Metalobosia</i>         |     |     |    |     |      |      |    |     |      |      |    |     |      |      |       |
| <i>diaxantha</i>           | 0   | 1   | 0  | 3   | 2    | 1    | 0  | 0   | 1    | 1    | 0  | 0   | 0    | 0    | 9     |
| <i>Nodozana coresa</i>     | 11  | 1   | 0  | 23  | 2    | 0    | 0  | 0   | 6    | 2    | 0  | 0   | 0    | 0    | 45    |
| <i>Praepiella sesapina</i> | 1   | 3   | 0  | 0   | 1    | 0    | 0  | 0   | 0    | 0    | 0  | 0   | 0    | 0    | 5     |
| <i>Pronola</i> spML01      | 0   | 4   | 0  | 7   | 10   | 11   | 0  | 0   | 1    | 3    | 0  | 0   | 0    | 0    | 36    |
| <i>Rhabdatomis</i>         |     |     |    |     |      |      |    |     |      |      |    |     |      |      |       |
| spML01                     | 2   | 1   | 0  | 2   | 4    | 2    | 0  | 0   | 3    | 1    | 0  | 0   | 0    | 0    | 15    |
| <i>Talara semiflava</i>    | 0   | 3   | 0  | 0   | 1    | 2    | 0  | 0   | 0    | 0    | 0  | 0   | 0    | 0    | 6     |
| <i>Talara</i> spML01       | 0   | 0   | 0  | 0   | 1    | 0    | 0  | 0   | 3    | 0    | 0  | 1   | 0    | 2    | 7     |
| <b>TOTAL</b>               | 109 | 58  | 11 | 341 | 524  | 318  | 11 | 44  | 1379 | 986  | 21 | 60  | 616  | 1313 | 5791  |
| <b>TOTAL</b>               | 434 | 501 | 34 | 862 | 1337 | 1316 | 55 | 368 | 3377 | 2168 | 35 | 181 | 1305 | 2053 | 14026 |

**Appendix 3I:** Sampling sites location of selected studies on arctiine diversity in different Brazilian biomes



|                 |                           |                     |                        |
|-----------------|---------------------------|---------------------|------------------------|
| Atlantic Forest | Teston and Corseuil, 2004 | Teston et al., 2006 | 12- Teston et al. 2010 |
| Amazon          | 1- Iraí                   | 7- Barracão         |                        |
| Pampa           | 2- Lagoa Vermelha         | 8- Sarandi          | 13- Teston et al. 2012 |
|                 | 3- São Pedro da Serra     | 9- Derrubadas       |                        |
|                 | 4- Camaquã                | 10- Alegrete        |                        |
|                 | 5- Mostardas              |                     |                        |
|                 | 6- Piratini               |                     |                        |
|                 |                           | 11- This study      |                        |

**Appendix 1III.** List of morphologically recognizable species and the species revealed by DNA barcoding (Rearrangements 1, 2, 3, and 4) classified according to the different types of rearrangements and their sources of disagreement.

| Taxa          | Morphological ly delimited species | Source of variation | Type of rearrangement   | Rearrangment 1                                      | Rearrangment 2                              | Rearrangment 3 | Rearrangment 4 |
|---------------|------------------------------------|---------------------|-------------------------|---|---|----------------|----------------|
| Lithosiini    | Agylla polysemata                  | ?                   | Clustering              | Agylla polysemata+Agylla sp. JAT02+Agylla sp. JAT05 |   |                |                |
| Lithosiini    | Agylla sp. JAT02                   | ?                   | Clustering              | Agylla sp. JAT02+Agylla sp. JAT05+Agylla polysemata |   |                |                |
| Lithosiini    | Agylla sp. JAT05                   | ?                   | Clustering              | Agylla sp. JAT05+Agylla sp. JAT02+Agylla polysemata |   |                |                |
| Lithosiini    | Agylla sp. JAT07                   | ?                   | Clustering              | Agylla sp. JAT07+Agylla sp. JAT08                   |   |                |                |
| Lithosiini    | Agylla sp. JAT08                   | ?                   | Break up and clustering | Agylla sp. JAT08+Agylla sp. JAT07                   | Agylla sp. JAT08                            |                |                |
| Ctenuchina    | Arctiinae sp. JAT03                | ?                   | Clustering              | Arctiinae sp. JAT03+Eucereon sp. JAT03              |   |                |                |
| Ctenuchina    | Eucereon sp. JAT03                 | ?                   | Clustering              | Eucereon sp. JAT03+Arctiinae sp. JAT03              |   |                |                |
| Ctenuchina    | Arctiinae sp. JAT07                | Sexual dimorphism   | Clustering              | Arctiinae sp. JAT07+Saurita sp. JAT01               |   |                |                |
| Euchromiina   | Saurita sp. JAT01                  | Sexual dimorphism   | Clustering              | Saurita sp. JAT01+Arctiinae sp. JAT07               |   |                |                |
| Phaegopterina | Arctiinae sp. JAT18                | Sexual dimorphism   | Clustering              | Arctiinae sp. JAT18+Leucanopsis sp. JAT08           |   |                |                |
| Phaegopterina | Leucanopsis sp. JAT08              | Sexual dimorphism   | Clustering              | Leucanopsis sp. JAT08+Arctiinae sp. JAT18           |   |                |                |
| Phaegopterina | Arctiinae sp. JAT25                | ?                   | Clustering              | Arctiinae sp. JAT25+Leucanopsis sp. JAT04           |   |                |                |
| Phaegopterina | Leucanopsis sp. JAT04              | ?                   | Break up and clustering | Leucanopsis sp. JAT04+Arctiinae sp. JAT25           | Leucanopsis sp. JAT04+Leucanopsis sp. JAT06 |                |                |
| Phaegopterina | Leucanopsis sp. JAT06              | ?                   | Clustering              | Leucanopsis sp. JAT06+Leucanopsis sp. JAT04         |   |                |                |
| Phaegopterina | Arctiinae sp. JAT30                | Sexual dimorphism   | Clustering              | Arctiinae sp. JAT30+Symphlebia perflua              |   |                |                |



|               |                        |                   |                         |   |                         |  |
|---------------|------------------------|-------------------|-------------------------|---|-------------------------|--|
| Phaegopterina | Symphlebia perflua     | Sexual dimorphism | Clustering              | Symphlebia perflua+Arctiinae sp. JAT30                        |                         |  |
| Phaegopterina | Arctiinae sp. JAT34    | ?                 | Clustering              | Arctiinae sp. JAT34+Arctiinae sp. JAT32+Leucanopsis sp. JAT02 |                         |  |
| Phaegopterina | Arctiinae sp. JAT32    | DNA barcode       | Break up and clustering | Arctiinae sp. JAT32+Arctiinae sp. JAT34+Leucanopsis sp. JAT02 | Arctiinae sp. JAT32     | Melese sp. JAT06+Melese incertus+Arctiinae sp. JAT32 |
| Phaegopterina | Leucanopsis sp. JAT02  | ?                 | Clustering              | Leucanopsis sp. JAT02+Arctiinae sp. JAT34+Arctiinae sp. JAT32 |                         |  |
| Ctenuchina    | Correbidia sp. JAT01   | ?                 | Clustering              | Correbidia sp. JAT01+Correbidia elegansMMZ02                  |                         |  |
| Ctenuchina    | Correbidia elegans     | ?                 | Break up and clustering | Correbidia elegansMMZ02+Correbidia sp. JAT01                  | Correbidia elegansMMZ01 |  |
| Ctenuchina    | Epidesma sp. JAT01     | ?                 | Clustering              | Epidesma sp. JAT01+Epidesma sp. JAT02                         |                         |  |
| Ctenuchina    | Epidesma sp. JAT02     | ?                 | Clustering              | Epidesma sp. JAT02+Epidesma sp. JAT01                         |                         |  |
| Lithosiini    | Illice sp. ML01        | ?                 | Clustering              | Illice sp. ML01+Illice brunea                                 |                         |  |
| Lithosiini    | Illice brunea          | ?                 | Break up and clustering | Illice brunea+Illice sp. ML01                                 | Illice brunea           |  |
| Lithosiini    | Lycomorphodes sp. ML01 | ?                 | Clustering              | Lycomorphodes sp. ML01+Lycomorphodes strigosa                 |                         |  |
| Lithosiini    | Lycomorphodes strigosa | ?                 | Clustering              | Lycomorphodes strigosa+Lycomorphodes sp. ML01                 |                         |  |
| Phaegopterina | Melese sp. JAT01       | Sexual dimorphism | Clustering              | Melese sp. JAT01+Melese sp. JAT03                             |                         |  |
| Phaegopterina | Melese sp. JAT03       | Sexual dimorphism | Clustering              | Melese sp. JAT03+Melese sp. JAT01                             |                         |  |
| Phaegopterina | Melese sp. JAT04       | Sexual dimorphism | Clustering              | Melese sp. JAT04+Melese sp. JAT11                             |                         |  |
| Phaegopterina | Melese sp.             | Sexual            | Clustering              | Melese sp. JAT11+Melese                                       |                         |  |

|               |                      |                   |                         |   |                                   |
|---------------|----------------------|-------------------|-------------------------|---|-----------------------------------|
|               | JAT11                | dimorphism        |                         | sp. JAT04   |                                   |
| Phaegopterina | Melese sp. JAT06     | ?                 | Clustering              | Melese sp. JAT06+Melese incertus+Melese sp. JAT12 |                                   |
| Phaegopterina | Melese incertus      | ?                 | Break up and clustering | Melese incertus+Melese sp. JAT06+Melese sp. JAT12 | Melese incertusMMZ01              |
| Phaegopterina | Melese sp. JAT12     | ?                 | Clustering              | Melese sp. JAT12+Melese sp. JAT06+Melese incertus |                                   |
| Phaegopterina | Melese sp. JAT07     | Sexual dimorphism | Clustering              | Melese sp. JAT07+Melese sp. JAT10                 |                                   |
| Phaegopterina | Melese sp. JAT10     | ?                 | Break up and clustering | Melese sp. JAT10+Melese castrena                  | Melese sp. JAT10+Melese sp. JAT07 |
| Phaegopterina | Melese castrena      | ?                 | Break up and clustering | Melese castrena+Melese sp. JAT08                  | Melese castrena+Melese sp. JAT10  |
| Phaegopterina | Melese sp. JAT08     | Sexual dimorphism | Clustering              | Melese sp. JAT08+Melese castrena                  |                                   |
| Phaegopterina | Pachydota sp. JAT01  | DNA barcode       | Clustering              | Pachydota sp. JAT01+Phaegoptera fuscaMMZ02        |                                   |
| Phaegopterina | Phaegoptera fusca    | DNA barcode       | Break up and clustering | Phaegoptera fuscaMMZ02+Pachydota sp. JAT01        | Phaegoptera fuscaMMZ001           |
| Phaegopterina | Symphlebia sp. JAT02 | Sexual dimorphism | Clustering              | Symphlebia sp. JAT02+Symphlebia distincta         |                                   |
| Phaegopterina | Symphlebia distincta | ?                 | Break up and clustering | Symphlebia distincta+Symphlebia sp. JAT02         | Symphlebia distinctaMMZ01         |
| Ctenuchina    | Aclytia terra        | OK                | OK                      | Aclytia terra                                     |                                   |
| Lithosiini    | Agylla sp. JAT01     | OK                | OK                      | Agylla sp. JAT01                                  |                                   |
| Lithosiini    | Agylla sp. JAT03     | OK                | OK                      | Agylla sp. JAT03                                  |                                   |
| Lithosiini    | Agylla sp. JAT04     | OK                | OK                      | Agylla sp. JAT04                                  |                                   |
| Lithosiini    | Agylla sp. JAT06     | OK                | OK                      | Agylla sp. JAT06                                  |                                   |
| Lithosiini    | Agylla sp. JAT09     | OK                | OK                      | Agylla sp. JAT09                                  |                                   |
| Lithosiini    | Agylla sp.           | OK                | OK                      | Agylla sp. JAT10                                  |                                   |

|               |                     |    |    |                     |
|---------------|---------------------|----|----|---------------------|
|               | JAT10               |    |    |                     |
| Lithosiini    | Agylla sp. JAT11    | OK | OK | Agylla sp. JAT11    |
| Lithosiini    | Agylla sp. JAT12    | OK | OK | Agylla sp. JAT12    |
| Lithosiini    | Agylla sp. JAT14    | OK | OK | Agylla sp. JAT14    |
| Ctenuchina    | Agyrta albisparsa   | OK | OK | Agyrta albisparsa   |
| Phaegopterina | Amasia corata       | OK | OK | Amasia corata       |
| Phaegopterina | Amasia hebe         | OK | OK | Amasia hebe         |
| Phaegopterina | Ammalo helops       | OK | OK | Ammalo helops       |
| Phaegopterina | Aphyle abdominalis  | OK | OK | Aphyle abdominalis  |
| Ctenuchina    | Arctiinae sp. JAT01 | OK | OK | Arctiinae sp. JAT01 |
| Ctenuchina    | Arctiinae sp. JAT02 | OK | OK | Arctiinae sp. JAT02 |
| Ctenuchina    | Arctiinae sp. JAT06 | OK | OK | Arctiinae sp. JAT06 |
| Euchromiina   | Arctiinae sp. JAT09 | OK | OK | Arctiinae sp. JAT09 |
| Euchromiina   | Arctiinae sp. JAT12 | OK | OK | Arctiinae sp. JAT12 |
| Euchromiina   | Arctiinae sp. JAT15 | OK | OK | Arctiinae sp. JAT15 |
| Phaegopterina | Arctiinae sp. JAT16 | OK | OK | Arctiinae sp. JAT16 |
| Phaegopterina | Arctiinae sp. JAT22 | OK | OK | Arctiinae sp. JAT22 |
| Phaegopterina | Arctiinae sp. JAT23 | OK | OK | Arctiinae sp. JAT23 |
| Phaegopterina | Arctiinae sp. JAT24 | OK | OK | Arctiinae sp. JAT24 |
| Phaegopterina | Arctiinae sp. JAT26 | OK | OK | Arctiinae sp. JAT26 |
| Phaegopterina | Arctiinae sp. JAT29 | OK | OK | Arctiinae sp. JAT29 |
| Phaegopterina | Arctiinae sp.       | OK | OK | Arctiinae sp. JAT33 |

|               |                         |    |    |                         |
|---------------|-------------------------|----|----|-------------------------|
|               | JAT33                   |    |    |                         |
| Phaegopterina | Arctiinae sp. JAT35     | OK | OK | Arctiinae sp. JAT35     |
| Phaegopterina | Arctiinae sp. JAT37     | OK | OK | Arctiinae sp. JAT37     |
| Lithosiini    | Arctiinae sp. JAT38     | OK | OK | Arctiinae sp. JAT38     |
| Lithosiini    | Arctiinae sp. JAT39     | OK | OK | Arctiinae sp. JAT39     |
| Lithosiini    | Arhabdosia sp. ML01     | OK | OK | Arhabdosia sp. ML01     |
| Euchromiina   | Erruca hanga            | OK | OK | Erruca hanga            |
| Ctenuchina    | Atypopsis sp. JAT01     | OK | OK | Atypopsis sp. JAT01     |
| Phaegopterina | Baritius acuminata      | OK | OK | Baritius acuminata      |
| Phaegopterina | Bernathonomus piperita  | OK | OK | Bernathonomus piperita  |
| Phaegopterina | Bertholdia pseudofumida | OK | OK | Bertholdia pseudofumida |
| Phaegopterina | Bertholdia soror        | OK | OK | Bertholdia soror        |
| Phaegopterina | Carales astur           | OK | OK | Carales astur           |
| Phaegopterina | Carathis byblis         | OK | OK | Carathis byblis         |
| Phaegopterina | Castrica phalaenoides   | OK | OK | Castrica phalaenoides   |
| Phaegopterina | Cissura decora          | OK | OK | Cissura decora          |
| Lithosiini    | Clemensia marmorata     | OK | OK | Clemensia marmorata     |
| Lithosiini    | Cloesia sp. ML01        | OK | OK | Cloesia sp. ML01        |
| Ctenuchina    | Correbidia lycoides     | OK | OK | Correbidia lycoides     |
| Euchromiina   | Cosmosoma centrale      | OK | OK | Cosmosoma centrale      |
| Euchromiina   | Cosmosoma durca         | OK | OK | Cosmosoma durca         |
| Euchromiina   | Cosmosoma elegans       | OK | OK | Cosmosoma elegans       |
| Euchromiina   | Cosmosoma               | OK | OK | Cosmosoma klagesi       |

|               |                         |    |    |                         |
|---------------|-------------------------|----|----|-------------------------|
|               | klagesi                 |    |    |                         |
| Euchromiina   | Cosmosoma leuconoton    | OK | OK | Cosmosoma leuconoton    |
| Euchromiina   | Cosmosoma plutona       | OK | OK | Cosmosoma plutona       |
| Euchromiina   | Cosmosoma sp. JAT01     | OK | OK | Cosmosoma sp. JAT01     |
| Euchromiina   | Cosmosoma sp. JAT02     | OK | OK | Cosmosoma sp. JAT02     |
| Euchromiina   | Cosmosoma sp. JAT04     | OK | OK | Cosmosoma sp. JAT04     |
| Euchromiina   | Cosmosoma teuthras      | OK | OK | Cosmosoma teuthras      |
| Phaegopterina | Cratoplastis catherinae | OK | OK | Cratoplastis catherinae |
| Phaegopterina | Delphyre flaviceps      | OK | OK | Delphyre flaviceps      |
| Phaegopterina | Delphyre sp. ML01       | OK | OK | Delphyre sp. ML01       |
| Euchromiina   | Dycladia lucetius       | OK | OK | Dycladia lucetius       |
| Pericopina    | Dysschema amphissa      | OK | OK | Dysschema amphissa      |
| Pericopina    | Dysschema fantasma      | OK | OK | Dysschema fantasma      |
| Pericopina    | Dysschema lucifer       | OK | OK | Dysschema lucifer       |
| Pericopina    | Dysschema sp. JAT01     | OK | OK | Dysschema sp. JAT01     |
| Phaegopterina | Echeta divisa           | OK | OK | Echeta divisa           |
| Phaegopterina | Echeta sp. JAT01        | OK | OK | Echeta sp. JAT01        |
| Phaegopterina | Elysium cingulata       | OK | OK | Elysium cingulata       |
| Phaegopterina | Elysium superba         | OK | OK | Elysium superba         |
| Ctenuchina    | Epidesma ursula         | OK | OK | Epidesma ursula         |
| Ctenuchina    | Episcepsis endodasia    | OK | OK | Episcepsis endodasia    |

|               |                          |    |    |                          |
|---------------|--------------------------|----|----|--------------------------|
| Ctenuchina    | Episcepsis venata        | OK | OK | Episcepsis venata        |
| Euchromiina   | Erruca cardinale         | OK | OK | Erruca cardinale         |
| Euchromiina   | Erruca deyroliei         | OK | OK | Erruca deyroliei         |
| Euchromiina   | Erruca sanguipuncta      | OK | OK | Erruca sanguipuncta      |
| Ctenuchina    | Eucereon apicalis        | OK | OK | Eucereon apicalis        |
| Ctenuchina    | Eucereon chalcodon       | OK | OK | Eucereon chalcodon       |
| Ctenuchina    | Eucereon discolor        | OK | OK | Eucereon discolor        |
| Ctenuchina    | Eucereon griseata        | OK | OK | Eucereon griseata        |
| Ctenuchina    | Eucereon quadricolor     | OK | OK | Eucereon quadricolor     |
| Ctenuchina    | Eucereon setosum         | OK | OK | Eucereon setosum         |
| Ctenuchina    | Eucereon sp. JAT01       | OK | OK | Eucereon sp. JAT01       |
| Ctenuchina    | Eucereon tarona          | OK | OK | Eucereon tarona          |
| Ctenuchina    | Galethalea pica          | OK | OK | Galethalea pica          |
| Phaegopterina | Graphea paramarmorea     | OK | OK | Graphea paramarmorea     |
| Euchromiina   | Heterodontia haematica   | OK | OK | Heterodontia haematica   |
| Euchromiina   | Holophaea erharda        | OK | OK | Holophaea erharda        |
| Ctenuchina    | Hyaleucerea vulnerata    | OK | OK | Hyaleucerea vulnerata    |
| Pericopina    | Hyalurga fenestrata      | OK | OK | Hyalurga fenestrata      |
| Pericopina    | Hyalurga sp. JAT01       | OK | OK | Hyalurga sp. JAT01       |
| Phaegopterina | Hyperandra appendiculata | OK | OK | Hyperandra appendiculata |
| Arctiini      | Hypercompe               | OK | OK | Hypercompe sp. JAT01     |

|               |                            |    |    |                         |
|---------------|----------------------------|----|----|-------------------------|
|               | sp. JAT01                  |    |    |                         |
| Lithosiini    | Hypermaepha<br>sp. ML01    | OK | OK | Hypermaepha sp. ML01    |
| Phaegopterina | Hypidalia<br>enervis       | OK | OK | Hypidalia enervis       |
| Euchromiina   | Ichoria<br>chalcomedusa    | OK | OK | Ichoria chalcomedusa    |
| Euchromiina   | Ichoria<br>tricincta       | OK | OK | Ichoria tricincta       |
| Lithosiini    | Illice<br>cryptopygra      | OK | OK | Illice cryptopygra      |
| Lithosiini    | Illice ditrigona           | OK | OK | Illice ditrigona        |
| Lithosiini    | Illice<br>endoxantha       | OK | OK | Illice endoxantha       |
| Lithosiini    | Illice sp.<br>ML05         | OK | OK | Illice sp. ML05         |
| Euchromiina   | Isanthrene<br>incendiaria  | OK | OK | Isanthrene incendiaria  |
| Phaegopterina | Ischnognatha<br>leucapera  | OK | OK | Ischnognatha leucapera  |
| Arctiini      | Isia alcumena              | OK | OK | Isia alcumena           |
| Phaegopterina | Lepidokirbyia<br>vittipes  | OK | OK | Lepidokirbyia vittipes  |
| Phaegopterina | Lepidozikania<br>sp. JAT01 | OK | OK | Lepidozikania sp. JAT01 |
| Phaegopterina | Leucanopsis<br>coniota     | OK | OK | Leucanopsis coniota     |
| Phaegopterina | Leucanopsis<br>leucanina   | OK | OK | Leucanopsis leucanina   |
| Phaegopterina | Leucanopsis<br>mandus      | OK | OK | Leucanopsis mandus      |
| Phaegopterina | Leucanopsis<br>oruba       | OK | OK | Leucanopsis oruba       |
| Phaegopterina | Leucanopsis<br>sp. JAT01   | OK | OK | Leucanopsis sp. JAT01   |
| Phaegopterina | Leucanopsis<br>sp. JAT03   | OK | OK | Leucanopsis sp. JAT03   |
| Phaegopterina | Leucanopsis<br>sp. JAT05   | OK | OK | Leucanopsis sp. JAT05   |
| Phaegopterina | Leucanopsis                | OK | OK | Leucanopsis sp. JAT07   |

|               |                              |    |    |                       |
|---------------|------------------------------|----|----|-----------------------|
| Phaegopterina | sp. JAT07<br>Lophocampa arpi | OK | OK | Lophocampa arpi       |
| Phaegopterina | Mazaeras francki             | OK | OK | Mazaeras francki      |
| Phaegopterina | Melese chozeba               | OK | OK | Melese chozeba        |
| Phaegopterina | Melese sp. JAT02             | OK | OK | Melese sp. JAT02      |
| Phaegopterina | Melese sp. JAT05             | OK | OK | Melese sp. JAT05      |
| Phaegopterina | Melese sp. JAT09             | OK | OK | Melese sp. JAT09      |
| Euchromiina   | Mirandisca harpalyce         | OK | OK | Mirandisca harpalyce  |
| Ctenuchina    | Napata sp. JAT01             | OK | OK | Napata sp. JAT01      |
| Phaegopterina | Neonerita dorsipuncta        | OK | OK | Neonerita dorsipuncta |
| Euchromiina   | Neotrichura nigripes         | OK | OK | Neotrichura nigripes  |
| Phaegopterina | Ochrodota pronapides         | OK | OK | Ochrodota pronapides  |
| Phaegopterina | Opharus basalis              | OK | OK | Opharus basalis       |
| Phaegopterina | Opharus brasiliensis         | OK | OK | Opharus brasiliensis  |
| Phaegopterina | Opharus notata               | OK | OK | Opharus notata        |
| Phaegopterina | Opharus procroides           | OK | OK | Opharus procroides    |
| Phaegopterina | Opharus rema                 | OK | OK | Opharus rema          |
| Phaegopterina | Ormetica iheringi            | OK | OK | Ormetica iheringi     |
| Phaegopterina | Ormetica rothschildi         | OK | OK | Ormetica rothschildi  |
| Arctiini      | Paracles sp. JAT02           | OK | OK | Paracles sp. JAT02    |
| Arctiini      | Paracles variegata           | OK | OK | Paracles variegata    |
| Phaegopterina | Pareuchaetes                 | OK | OK | Pareuchaetes sp. ML01 |



|               |                                |    |    |                                |
|---------------|--------------------------------|----|----|--------------------------------|
|               | sp. ML01                       |    |    |                                |
| Phaegopterina | Pelochyta sp. JAT01            | OK | OK | Pelochyta sp. JAT01            |
| Phaegopterina | Phaegoptera chorima            | OK | OK | Phaegoptera chorima            |
| Phaegopterina | Phaegoptera histrionica        | OK | OK | Phaegoptera histrionica        |
| Ctenuchina    | Philoros affinis               | OK | OK | Philoros affinis               |
| Euchromiina   | Phoenicoprocta haemorrhoidalis | OK | OK | Phoenicoprocta haemorrhoidalis |
| Lithosiini    | Pronola sp. ML01               | OK | OK | Pronola sp. ML01               |
| Ctenuchina    | Pseudosphex rubripalpus        | OK | OK | Pseudosphex rubripalpus        |
| Euchromiina   | Psilopleura sanguipuncta       | OK | OK | Psilopleura sanguipuncta       |
| Lithosiini    | Rhabdatomis sp. ML01           | OK | OK | Rhabdatomis sp. ML01           |
| Phaegopterina | Rhipha flavithorax             | OK | OK | Rhipha flavithorax             |
| Phaegopterina | Rhipha subflammans             | OK | OK | Rhipha subflammans             |
| Euchromiina   | Rhynchopyga meisteri           | OK | OK | Rhynchopyga meisteri           |
| Phaegopterina | Robinsonia spitzi              | OK | OK | Robinsonia spitzi              |
| Euchromiina   | Sarosa sp. ML01                | OK | OK | Sarosa sp. ML01                |
| Phaegopterina | Scaptius sp. ML01              | OK | OK | Scaptius sp. ML01              |
| Phaegopterina | Selenarctia elissa             | OK | OK | Selenarctia elissa             |
| Pericopina    | Stenognatha gentilis           | OK | OK | Stenognatha gentilis           |
| Phaegopterina | Sychesia dryas                 | OK | OK | Sychesia dryas                 |
| Phaegopterina | Symphlebia lophocampoid        | OK | OK | Symphlebia lophocampoides      |

|               |                          |             |                         |  |  |                           |
|---------------|--------------------------|-------------|-------------------------|--|--|---------------------------|
| Lithosiini    | es<br>Talara semiflava   | OK          | OK                      | Talara semiflava                           |  |                           |
| Lithosiini    | Talara sp. ML01          | OK          | OK                      | Talara sp. ML01                            |  |                           |
| Phaegopterina | Thysanoprymna pyrrhopyga | OK          | OK                      | Thysanoprymna pyrrhopyga                   |  |                           |
| Phaegopterina | Trichromia sp. JAT05     | OK          | OK                      | Trichromia sp. JAT05                       |  |                           |
| Phaegopterina | Trichromia sp. JAT06     | DNA barcode | Break up and clustering | Trichromia sp. JAT06(1)+Eucereon sp. JAT02 | Trichromia sp. JAT06(2)+Eucereon sp. JAT02 | Trichromia sp. JAT06      |
| Phaegopterina | Tricypha imperialis      | OK          | OK                      | Tricypha imperialis                        |  |                           |
| Phaegopterina | Tricypha sp. JAT01       | OK          | OK                      | Tricypha sp. JAT01                         |  |                           |
| Phaegopterina | Viviennea dolens         | OK          | OK                      | Viviennea dolens                           |  |                           |
| Phaegopterina | Viviennea moma           | OK          | OK                      | Viviennea moma                             |  |                           |
| Phaegopterina | Xanthophaeina levis      | OK          | OK                      | Xanthophaeina levis                        |  |                           |
| Phaegopterina | Agaraea semivitrea       | ?           | Break up                | Agaraea semivitreaMMZ01                    | Agaraea semivitreaMMZ02                    |                           |
| Phaegopterina | Arctiinae sp. JAT27      | Morphology  | Break up                | Arctiinae sp. 27 MMZ01                     | Arctiinae sp. 27 MMZ02                     |                           |
| Phaegopterina | Arctiinae sp. JAT28      | ?           | Break up                | Arctiinae sp. JAT28MMZ01                   | Arctiinae sp. JAT28MMZ02                   |                           |
| Phaegopterina | Baritius sp. ML01        | Morphology  | Break up                | Baritius sp. ML01MMZ01                     | Baritius sp. ML01MMZ02                     |                           |
| Euchromiina   | Cosmosoma auge           | ?           | Break up                | Cosmosoma augeMMZ01                        | Cosmosoma augeMMZ02                        |                           |
| Pericopina    | Dysschema hilarina       | ?           | Break up                | Dysschema hilarinaMMZ01                    | Dysschema hilarinaMMZ02                    |                           |
| Phaegopterina | Elysia pyrosticta        | Morphology  | Break up                | Elysia pyrostictaMMZ01                     | Elysia pyrostictaMMZ02                     |                           |
| Ctenuchina    | Eucereon rosa            | Morphology  | Break up                | Eucereon rosaMMZ01                         | Eucereon rosaMMZ02                         |                           |
| Ctenuchina    | Euceriodes wernickei     | ?           | Break up                | Euceriodes wernickeiMMZ01                  | Euceriodes wernickeiMMZ02                  | Euceriodes wernickeiMMZ03 |

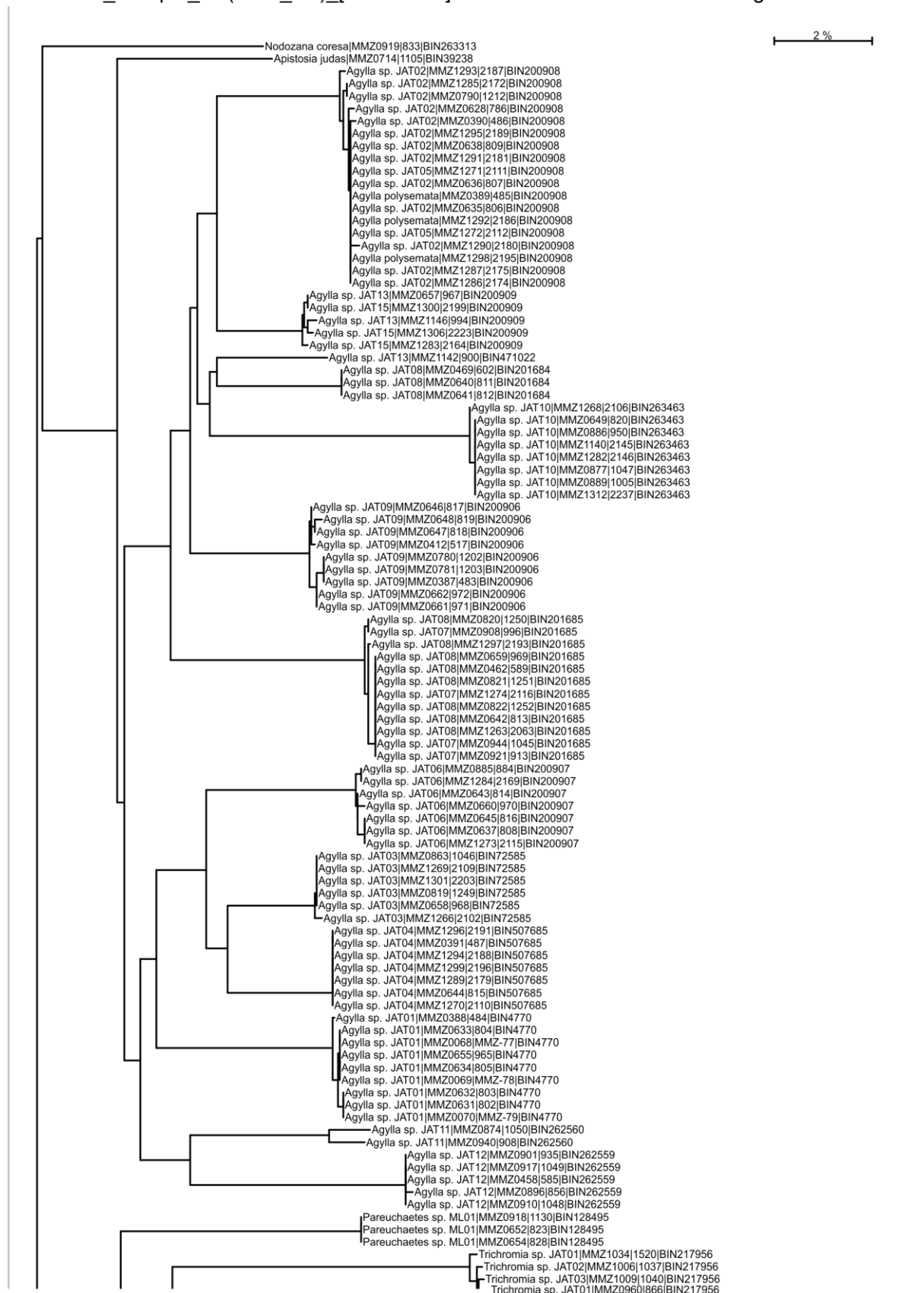
|               |                         |                   |                         |                              |                              |                        |                      |
|---------------|-------------------------|-------------------|-------------------------|------------------------------|------------------------------|------------------------|----------------------|
| Phaegopterina | Eupseudosoma involuta   | Morphology        | Break up                | Eupseudosoma involutaMMZ01   | Eupseudosoma involutaMMZ02   |                        |                      |
| Phaegopterina | Idalus lineosus         | ?                 | Break up                | Idalus lineosusMMZ01         | Idalus lineosusMMZ02         | Idalus lineosusMMZ03   |                      |
| Lithosiini    | Illice sp. ML04         | ?                 | Break up                | Illice sp. ML04MMZ01         | Illice sp. ML04MMZ02         |                        |                      |
| Phaegopterina | Ischnocampa lugubris    | Morphology        | Break up                | Ischnocampa lugubrisMMZ01    | Ischnocampa lugubrisMMZ02    |                        |                      |
| Phaegopterina | Lophocampa sp. JAT01    | Morphology        | Break up                | Lophocampa sp. JAT01MMZ01    | Lophocampa sp. JAT01MMZ02    |                        |                      |
| Phaegopterina | Lophocampa sp. JAT02    | ?                 | Break up                | Lophocampa sp. JAT02MMZ01    | Lophocampa sp. JAT02MMZ02    |                        |                      |
| Phaegopterina | Lophocampa texta        | Morphology        | Break up                | Lophocampa textaMMZ01        | Lophocampa textaMMZ02        |                        |                      |
| Phaegopterina | Machadoia xanthosticta  | Morphology        | Break up                | Machadoia xanthostictaMMZ01  | Machadoia xanthostictaMMZ02  |                        |                      |
| Euchromiina   | Macrocneme sp. JAT01    | ?                 | Break up                | Macrocneme sp. JAT01         | Macrocneme sp. JAT02         | Macrocneme sp. JAT03   | Macrocneme sp. JAT04 |
| Euchromiina   | Mesothera desperata     | Morphology        | Break up                | Mesothera desperataMMZ01     | Mesothera desperataMMZ02     |                        |                      |
| Lithosiini    | Metalobosia diaxantha   | Morphology        | Break up                | Metalobosia diaxanthaMMZ01   | Metalobosia diaxanthaMMZ02   |                        |                      |
| Lithosiini    | Nodozana coresa         | ?                 | Break up                | Nodozana coresaMMZ01         | Nodozana coresaMMZ02         |                        |                      |
| Phaegopterina | Pachydota affinis       | Morphology        | Break up                | Pachydota affinisMMZ01       | Pachydota affinisMMZ02       | Pachydota affinisMMZ03 |                      |
| Arctiini      | Paracles fusca          | ?                 | Break up                | Paracles fuscaMMZ01          | Paracles fuscaMMZ02          | Paracles fuscaMMZ03    |                      |
| Phaegopterina | Pelochyta cinerea       | ?                 | Break up                | Pelochyta cinereaMMZ01       | Pelochyta cinereaMMZ02       |                        |                      |
| Euchromiina   | Poliopastea indistincta | Morphology        | Break up                | Poliopastea indistinctaMMZ01 | Poliopastea indistinctaMMZ02 |                        |                      |
| Ctenuchina    | Theages leucophaea      | ?                 | Break up                | Theages leucophaeaMMZ01      | Theages leucophaeaMMZ02      |                        |                      |
| Arctiini      | Virbia divisa           | ?                 | Break up                | Virbia divisaMMZ01           | Virbia divisaMMZ02           |                        |                      |
| Ctenuchina    | Aclytia heber           | Sexual dimorphism | Clustering              | Aclytia heber+Aclytia jonesi |                              |                        |                      |
| Ctenuchina    | Aclytia jonesi          | ?                 | Break up and clustering | Aclytia jonesi+Aclytia heber | Aclytia jonesiMMZ01          |                        |                      |

|               |                           |                      |                            |   |  |                                 |
|---------------|---------------------------|----------------------|----------------------------|---|--|---------------------------------|
| Ctenuchina    | Aclytia sp.<br>JAT01      | Sexual<br>dimorphism | Clustering                 | Aclytia sp. JAT01+Aclytia<br>sp. JAT02+Eucereon sp.<br>JAT04            |  |                                 |
| Ctenuchina    | Aclytia sp.<br>JAT02      | Morphology           | Clustering                 | Aclytia sp. JAT02+Aclytia<br>sp. JAT01+Eucereon sp.<br>JAT04            |  |                                 |
| Ctenuchina    | Eucereon sp.<br>JAT04     | Sexual<br>dimorphism | Clustering                 | Eucereon sp. JAT04+Aclytia<br>sp. JAT01+Aclytia sp.<br>JAT02            |  |                                 |
| Lithosiini    | Agylla sp.<br>JAT13       | ?                    | Break up and<br>clustering | Agylla sp. JAT13+Agylla sp.<br>JAT15                                    | Agylla sp. JAT13   |                                 |
| Lithosiini    | Agylla sp.<br>JAT15       | ?                    | Clustering                 | Agylla sp. JAT15+Agylla sp.<br>JAT13                                    |  |                                 |
| Ctenuchina    | Episcea<br>extravagans    | DNA barcode          | Break up and<br>clustering | Episcea<br>extravagansMMZ01+Euchlae<br>nidia transcisaMMZ01             | Episcea<br>extravagansMMZ02  | Episcea<br>extravagansMMZ<br>03 |
| Ctenuchina    | Eucereon sp.<br>JAT02     | DNA barcode          | Break up and<br>clustering | Eucereon sp.<br>JAT02+Trichromia sp.<br>JAT06(1)                        | Eucereon sp.<br>JAT02+Trichromia<br>sp. JAT06(2)                           |                                 |
| Pericopina    | Euchlaenidia<br>transcisa | DNA barcode          | Clustering                 | Euchlaenidia<br>transcisaMMZ02+Episcea<br>extravagansMMZ01              |  |                                 |
| Phaegopterina | Idalus agastus            | ?                    | Break up and<br>clustering | Idalus agastus+Idalus sp.<br>JAT01MMZ01                                 | Idalus<br>agastusMMZ02   | Idalus<br>agastusMMZ03          |
| Phaegopterina | Idalus sp.<br>JAT01       | ?                    | Break up and<br>clustering | Idalus agastus+Idalus sp.<br>JAT01MMZ01                                 | Idalus sp.<br>JAT01MMZ02   |                                 |
| Phaegopterina | Trichromia sp.<br>JAT01   | ?                    | Break up and<br>clustering | Trichromia sp.<br>JAT01+Trichromia sp.<br>JAT02+Trichormia sp.<br>JAT03 | Trichromia sp.<br>JAT01+Trichromia<br>sp.<br>JAT02+Trichormia<br>sp. JAT04 |                                 |
| Phaegopterina | Trichromia sp.<br>JAT02   | ?                    | Break up and<br>clustering | Trichromia sp.<br>JAT01+Trichromia sp.<br>JAT02+Trichormia sp.<br>JAT03 | Trichromia sp.<br>JAT01+Trichromia<br>sp.<br>JAT02+Trichormia<br>sp. JAT04 |                                 |
| Phaegopterina | Trichromia sp.<br>JAT03   | ?                    | Clustering                 | Trichromia sp.<br>JAT01+Trichromia sp.<br>JAT02+Trichormia sp.<br>JAT03 |  |                                 |

|               |                         |   |            |   |
|---------------|-------------------------|---|------------|---|
| Phaegopterina | Trichromia sp.<br>JAT04 | ? | Clustering | Trichromia sp.<br>JAT01+Trichromia sp.<br>JAT02+Trichormia sp.<br>JAT04 |
|---------------|-------------------------|---|------------|---|

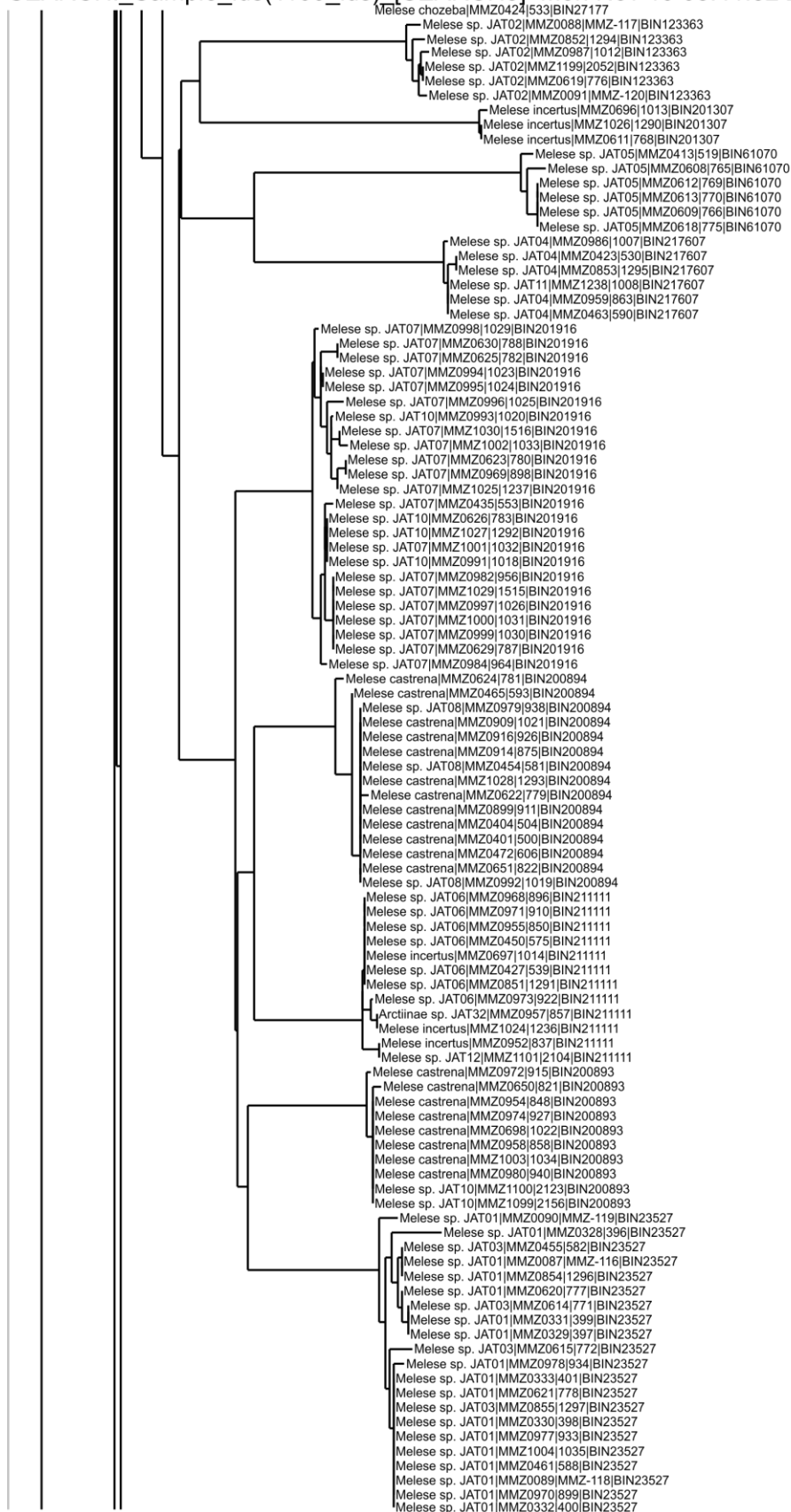
## **Appendix 2III:** Neighbor Joining

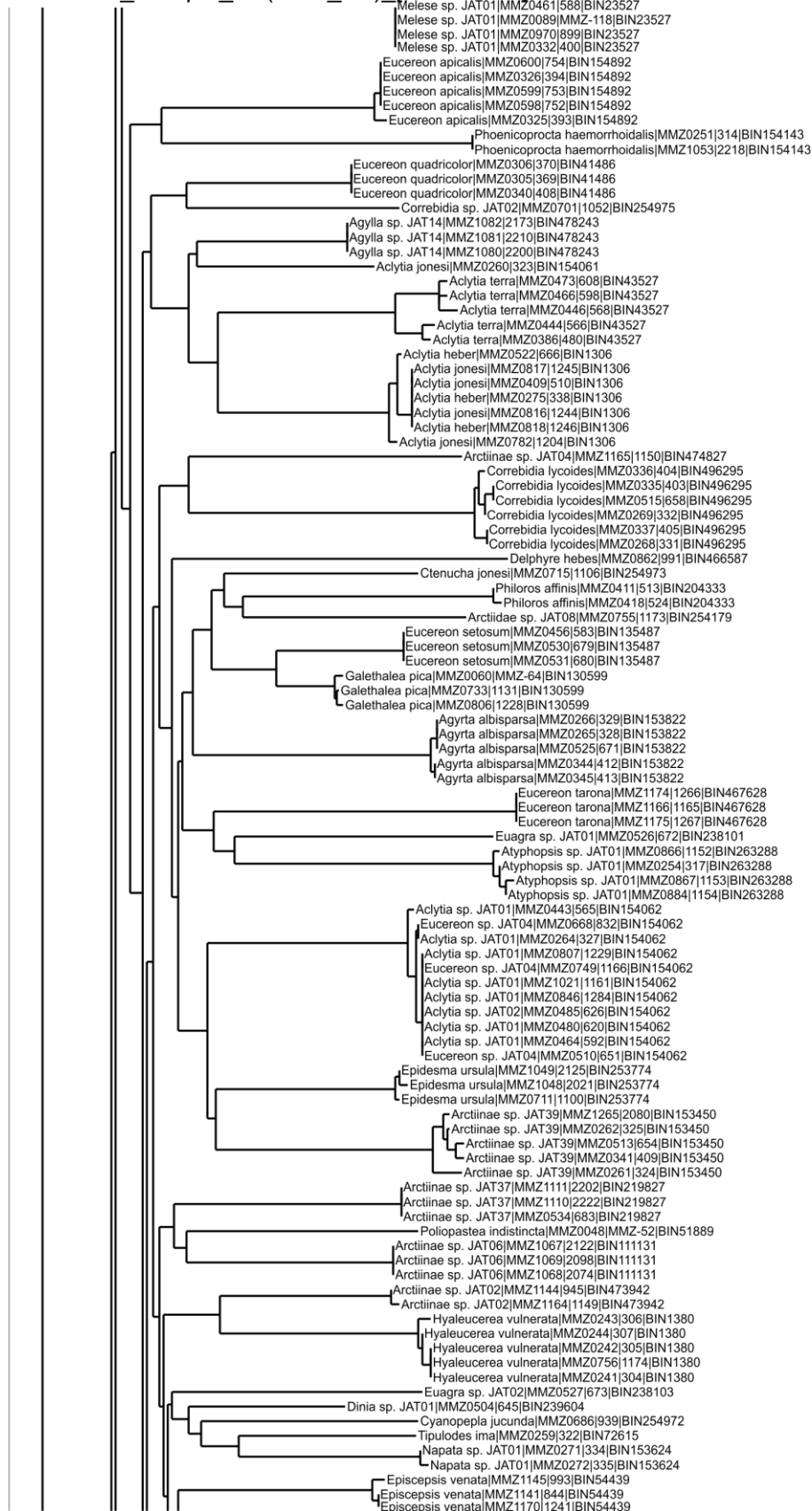
phenogram

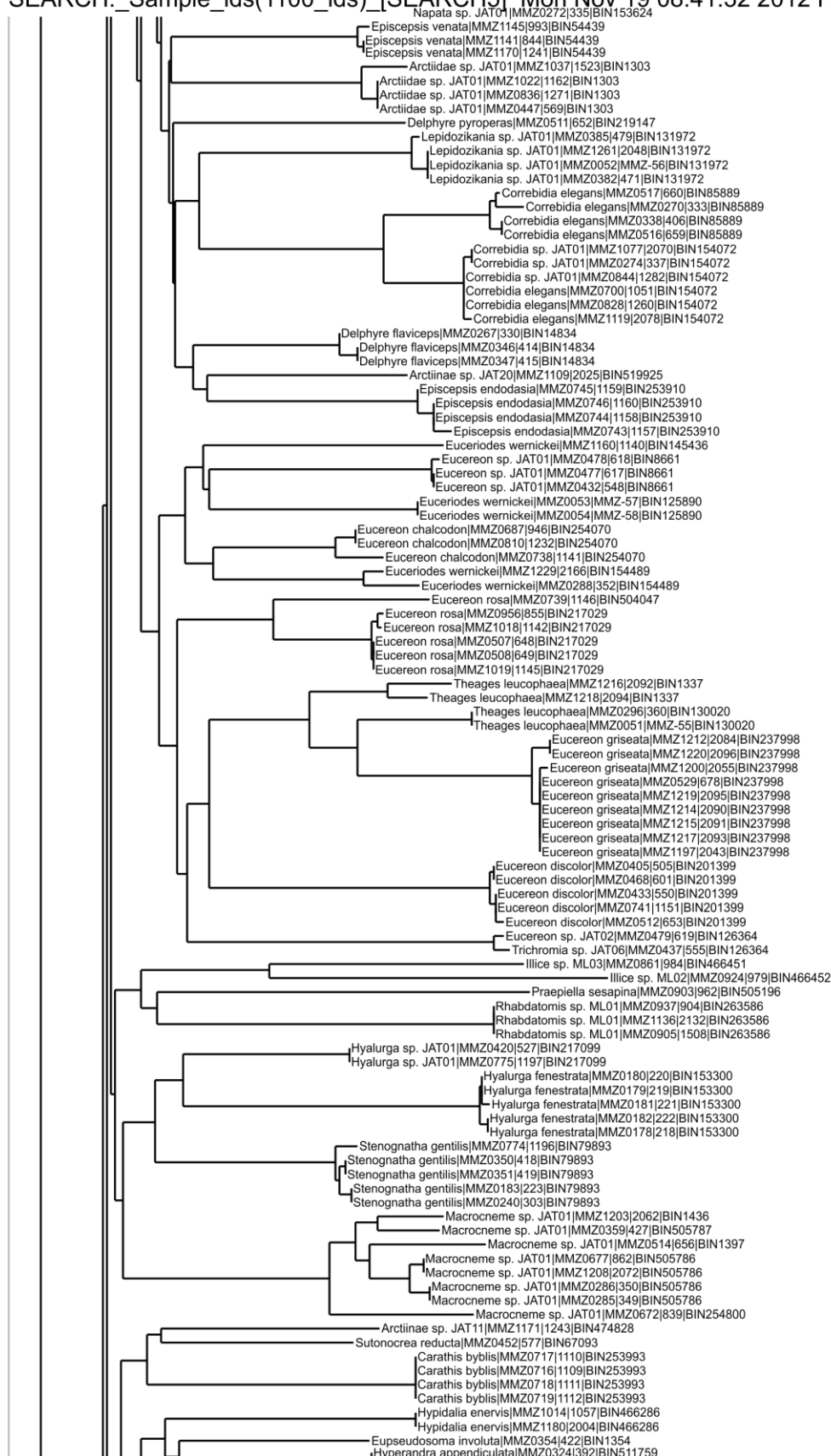


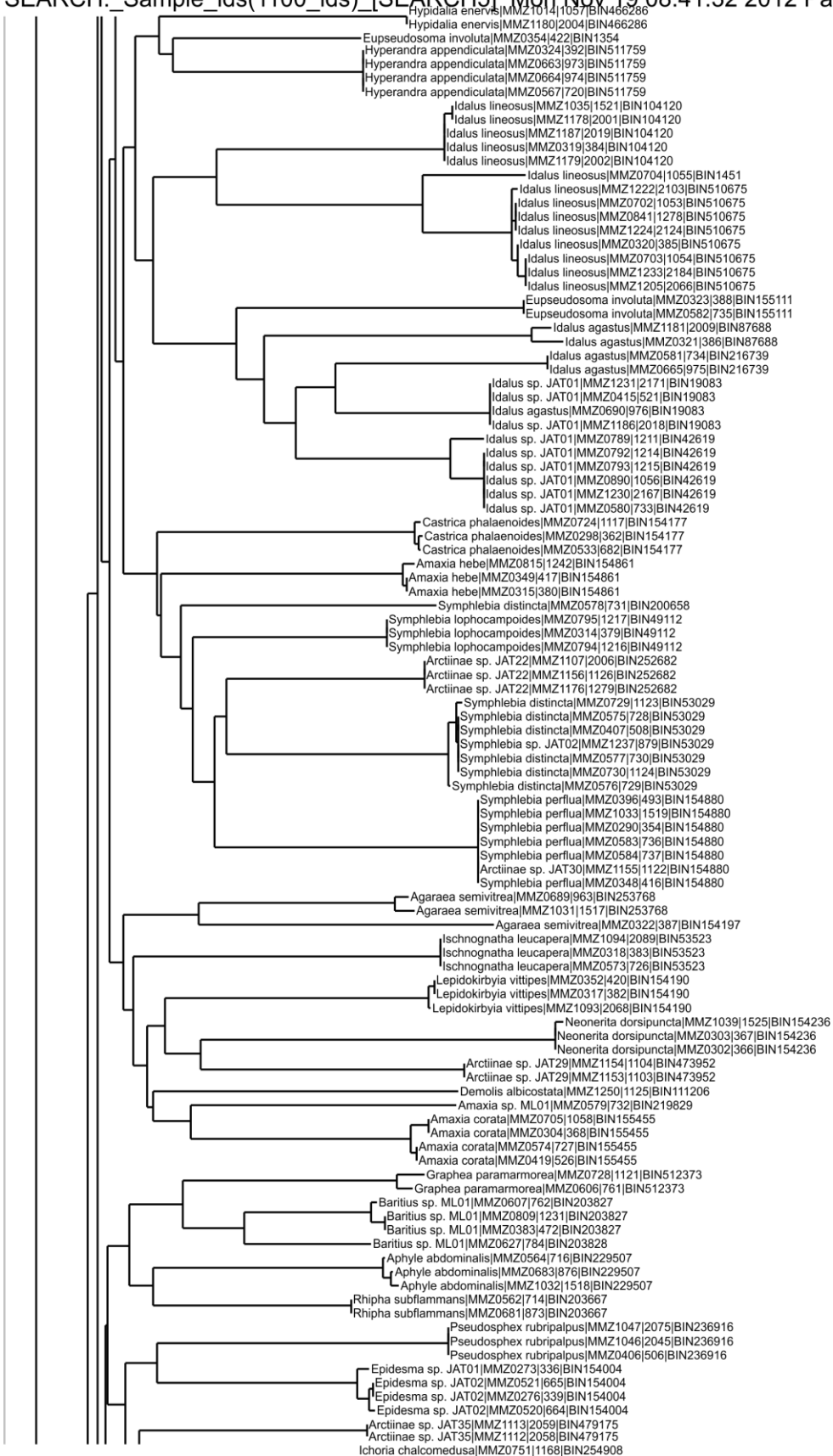


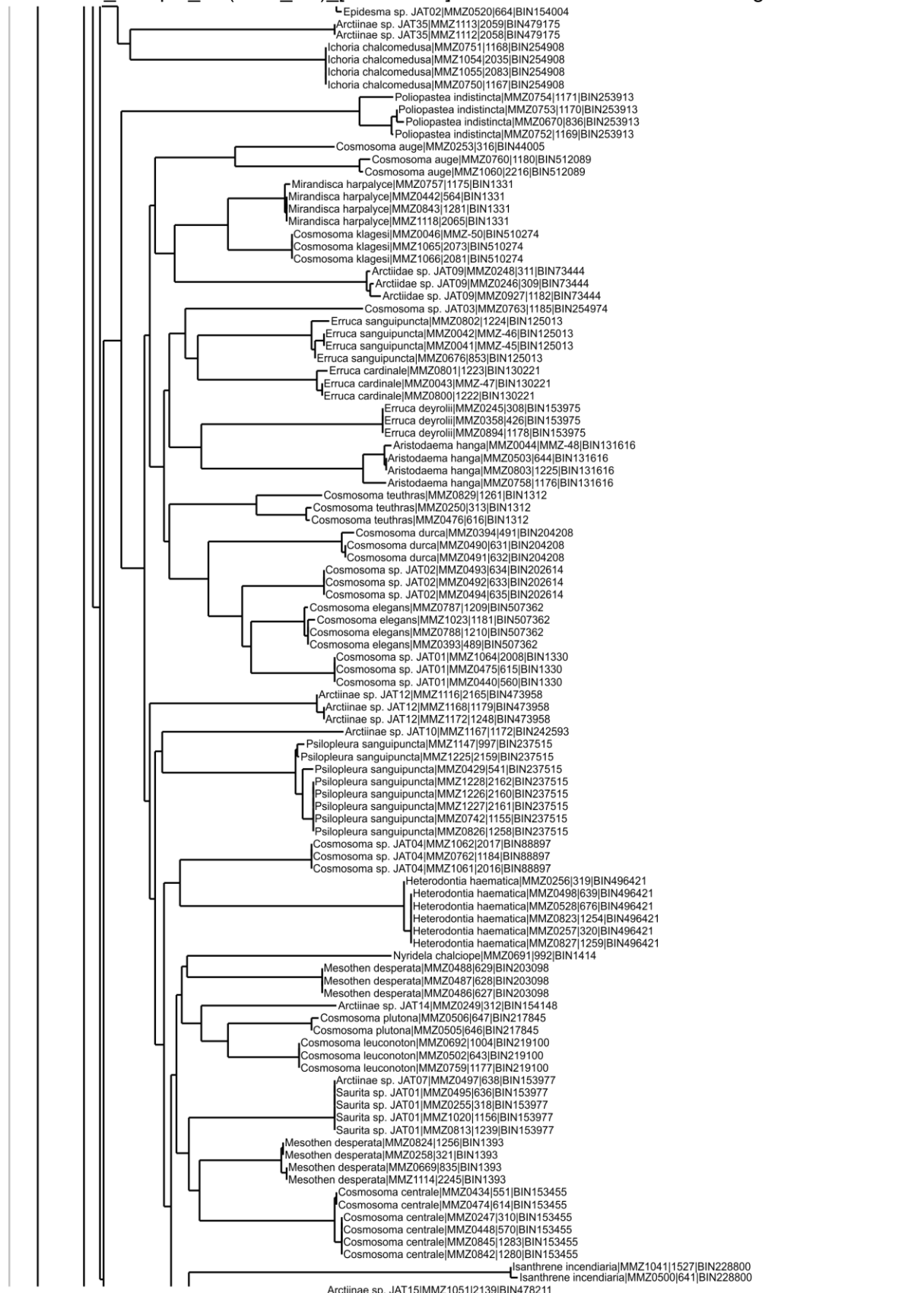


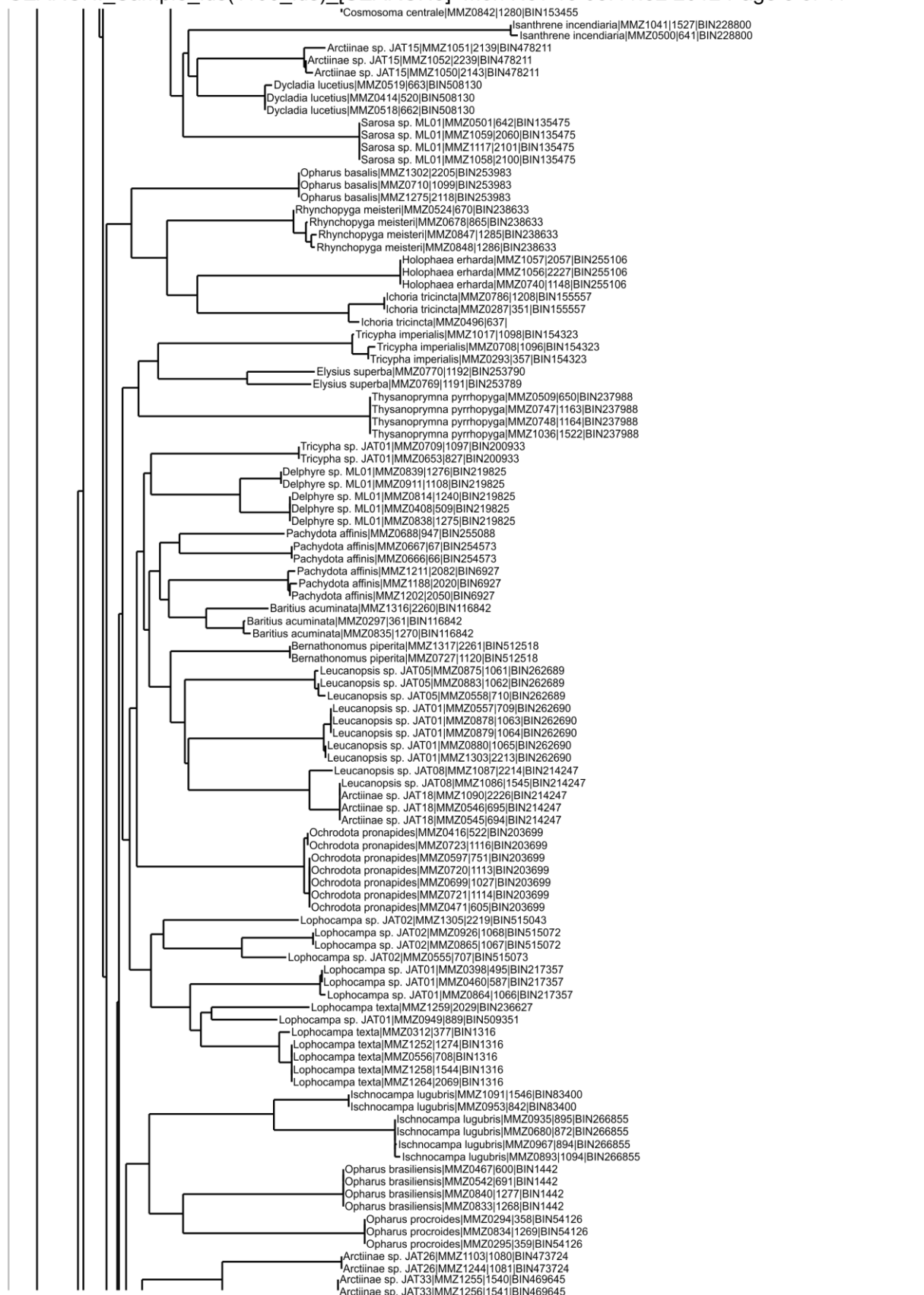


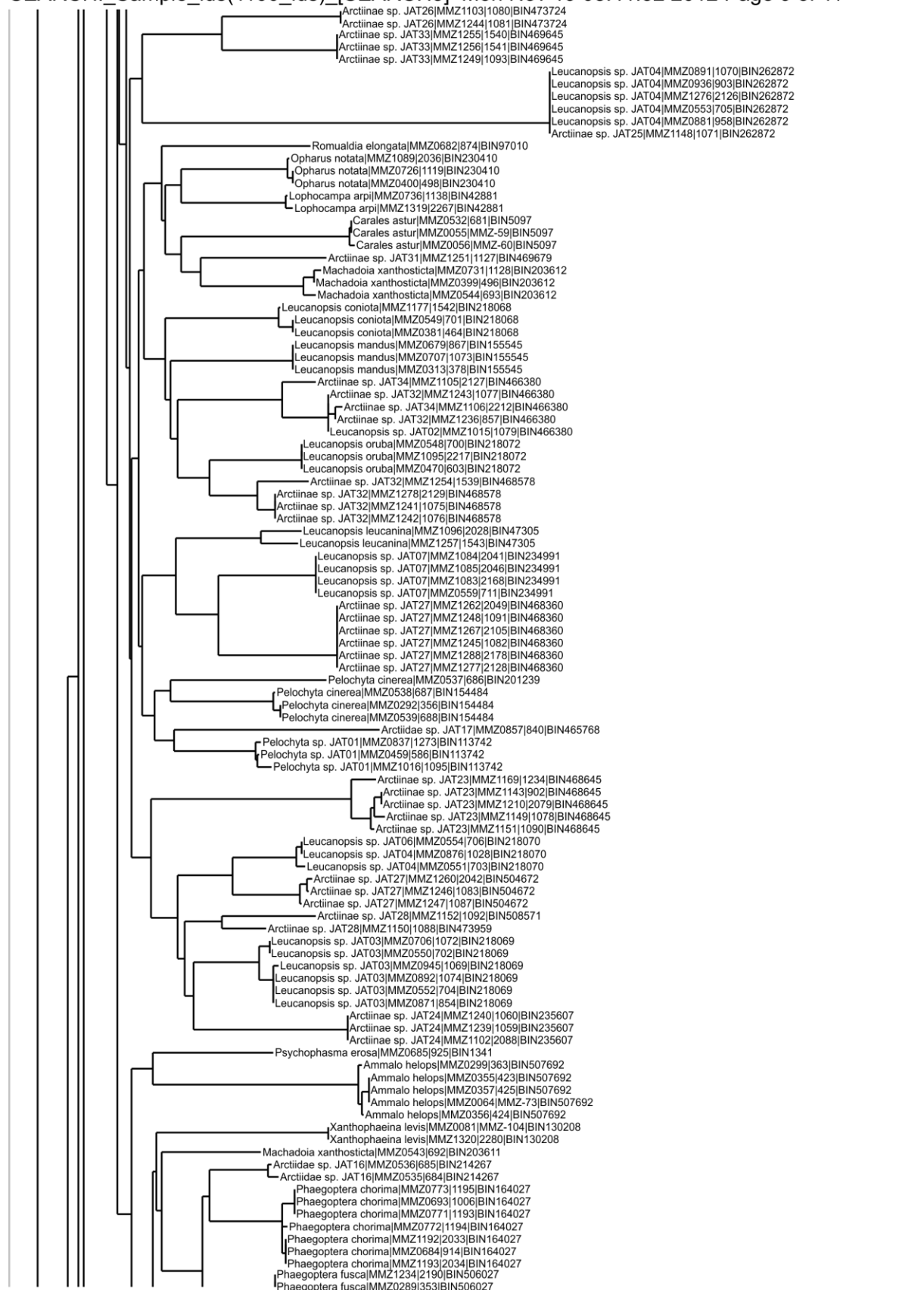


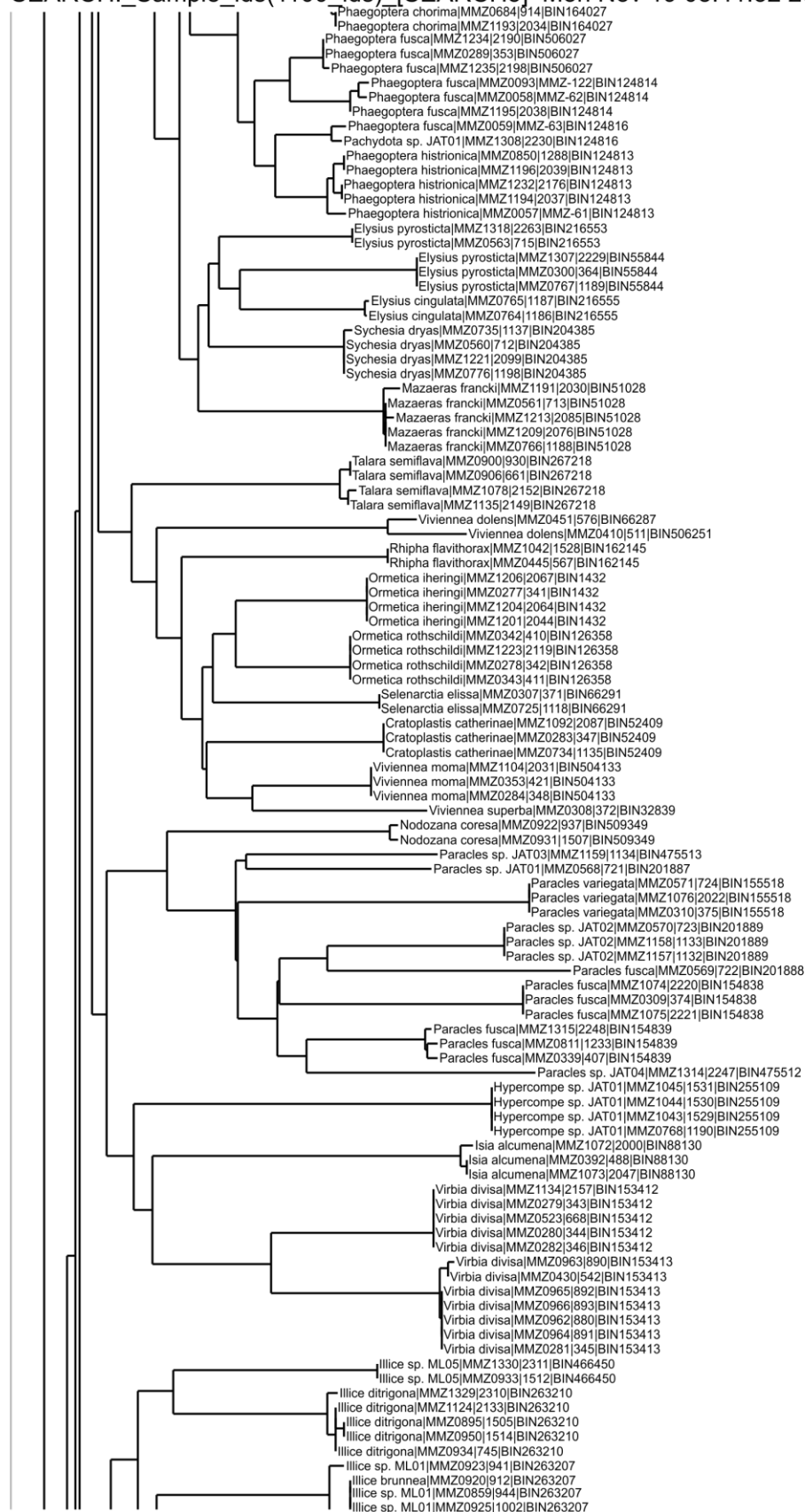




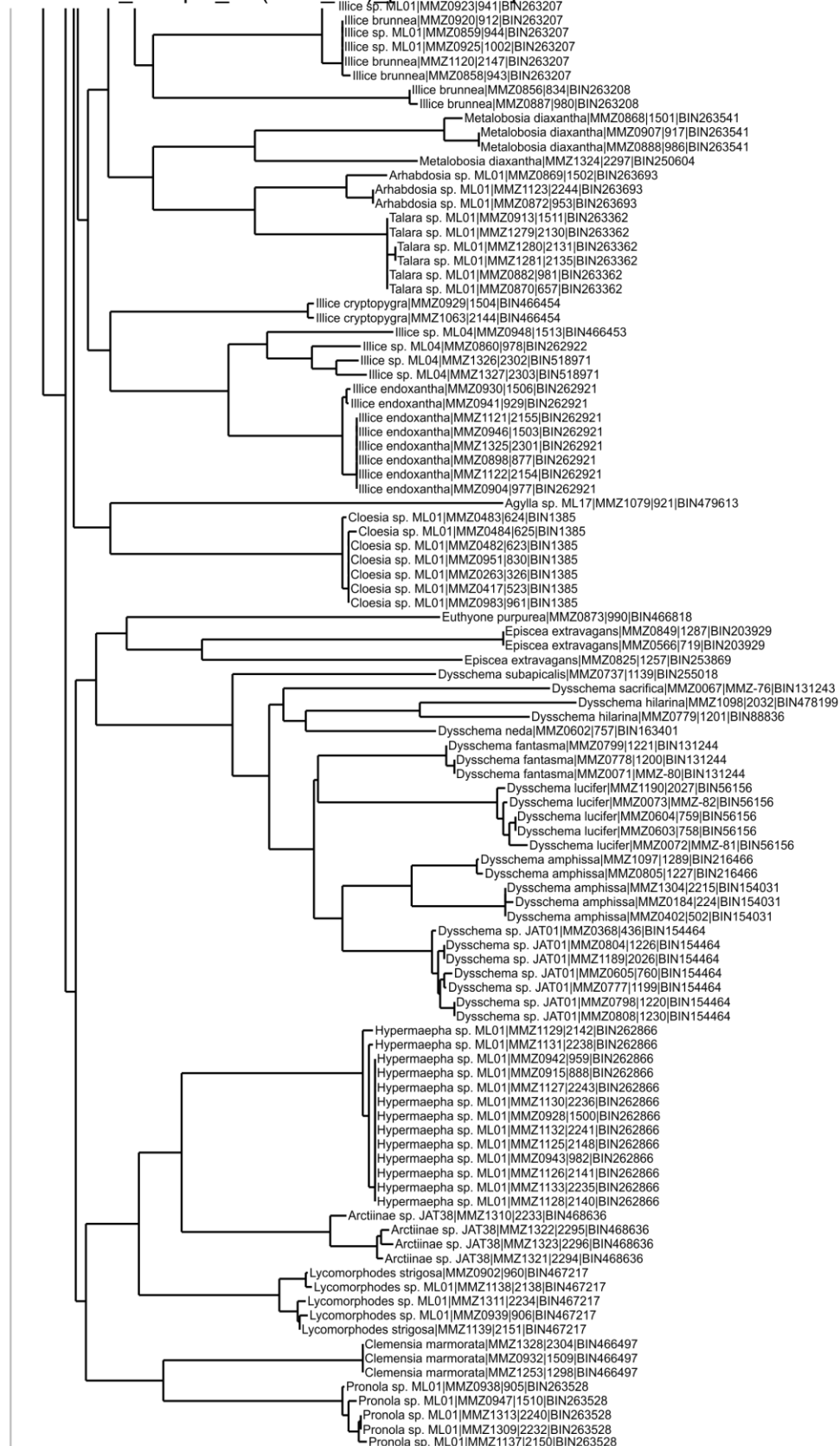












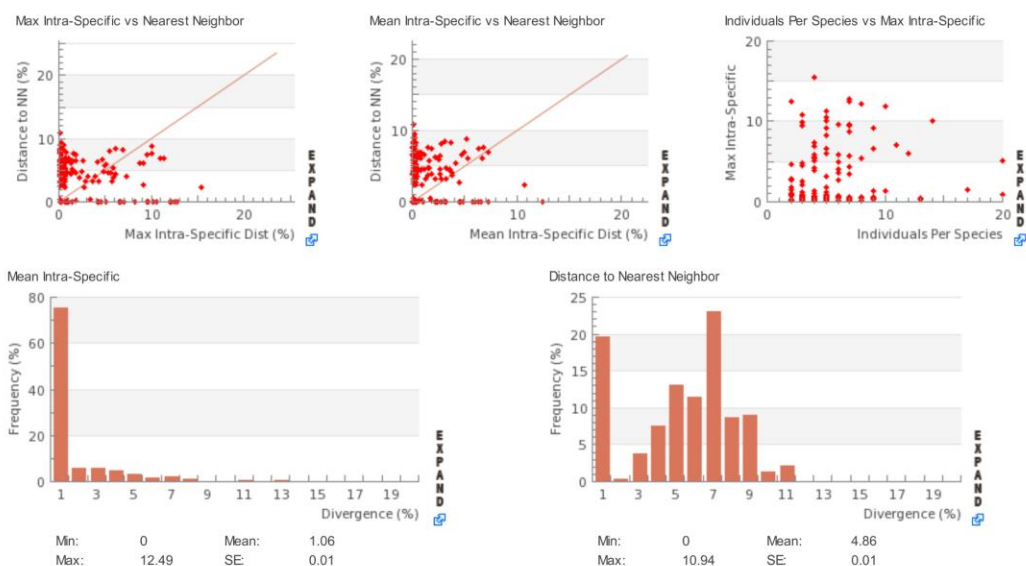
### **Appendix 3III: Barcode gap analysis**

## Barcode Gap Analysis Result - SEARCH: Sample ids(1100 ids)

Print

Number of Sequences: 1100  
 Species with high intra-specific distance (>2%): 73  
 Species with low distance to another species (<2%): 58

Show Warnings Only



| Order       | Family    | Species                | Mean Intra-Sp | Max Intra-Sp | Nearest Species        | Nearest Neighbor | Distance to NN |
|-------------|-----------|------------------------|---------------|--------------|------------------------|------------------|----------------|
| Lepidoptera | Arctiidae | Aclytia heber          | 0.2           | 0.31         | Aclytia jonesi         | LEMMZ817-11      | 0              |
| Lepidoptera | Arctiidae | Aclytia jonesi         | 2.72          | 6.58         | Aclytia heber          | LEMMZ275-10      | 0              |
| Lepidoptera | Arctiidae | Aclytia sp. JAT01      | 0.12          | 0.31         | Eucereon sp. JAT04     | LEMMZ510-11      | 0              |
| Lepidoptera | Arctiidae | Aclytia sp. JAT02      | N/A           | N/A          | Eucereon sp. JAT04     | LEMMZ510-11      | 0              |
| Lepidoptera | Arctiidae | Aclytia terra          | 1.12          | 1.87         | Aclytia heber          | LEMMZ522-11      | 6.58           |
| Lepidoptera | Arctiidae | Agyrtia albisparsa     | 0.09          | 0.15         | Galethalea pica        | LEMMZ733-11      | 6.56           |
| Lepidoptera | Arctiidae | Argyrodes sanguinea    | N/A           | N/A          | Melese sp. JAT09       | LEMMZ989-11      | 6.05           |
| Lepidoptera | Arctiidae | Athyopsis sp. JAT01    | 0.26          | 0.46         | Galethalea pica        | LEMMZ733-11      | 8.25           |
| Lepidoptera | Arctiidae | Cyanopepla jucunda     | N/A           | N/A          | Dinia sp. JAT01        | LEMMZ504-11      | 6.41           |
| Lepidoptera | Arctiidae | Dinia sp. JAT01        | N/A           | N/A          | Aglyia sp. JAT14       | LEMMZ1082-12     | 5.39           |
| Lepidoptera | Arctiidae | Dycladia lucetius      | 0.1           | 0.15         | Mesothene desperata    | LEMMZ258-10      | 3.29           |
| Lepidoptera | Arctiidae | Epidesma sp. JAT01     | N/A           | N/A          | Epidesma sp. JAT02     | LEMMZ276-10      | 0.48           |
| Lepidoptera | Arctiidae | Epidesma sp. JAT02     | 0.1           | 0.15         | Epidesma sp. JAT01     | LEMMZ273-10      | 0.48           |
| Lepidoptera | Arctiidae | Epidesma ursula        | 0.2           | 0.31         | Tipulodes ima          | LEMMZ259-10      | 6.51           |
| Lepidoptera | Arctiidae | Episcea extravagans    | 10.72         | 15.42        | Euchlaenidia transcisa | LEMMZ784-11      | 2.34           |
| Lepidoptera | Arctiidae | Euagra sp. JAT01       | N/A           | N/A          | Cyanopepla jucunda     | LEMMZ686-11      | 7.92           |
| Lepidoptera | Arctiidae | Euagra sp. JAT02       | N/A           | N/A          | Aglyia sp. JAT14       | LEMMZ1082-12     | 6.9            |
| Lepidoptera | Arctiidae | Euchlaenidia transcisa | 0.98          | 2.77         | Episcea extravagans    | LEMMZ785-11      | 2.34           |
| Lepidoptera | Arctiidae | Hyalocerea vulnerata   | 0.21          | 0.46         | Arctiinae sp. JAT02    | LEMMZ1144-12     | 6.56           |
| Lepidoptera | Arctiidae | Hyalurga fenestrata    | 0.15          | 0.31         | Hyalurga sp. JAT01     | LEMMZ775-11      | 8.31           |
| Lepidoptera | Arctiidae | Hyalurga sp. JAT01     | 0             | 0            | Pelochyta sp. JAT01    | LEMMZ837-11      | 6.21           |
| Lepidoptera | Arctiidae | Ichoria chalcamedusa   | 0             | 0            | Pelochyta sp. JAT01    | LEMMZ459-11      | 6.38           |
| Lepidoptera | Arctiidae | Ichoria tricineta      | 0.64          | 1.25         | Rhynchopyga meisteri   | LEMMZ524-11      | 6.22           |
| Lepidoptera | Arctiidae | Isanthrene incendiaria | 0.17          | 0.17         | Dycladia lucetius      | LEMMZ519-11      | 8.29           |
| Lepidoptera | Arctiidae | Mesothene desperata    | 3.26          | 5.74         | Dycladia lucetius      | LEMMZ518-11      | 3.29           |
| Lepidoptera | Arctiidae | Napata sp. JAT01       | 0.15          | 0.15         | Galethalea pica        | LEMMZ733-11      | 5.75           |
| Lepidoptera | Arctiidae | Nyrdela chalciope      | N/A           | N/A          | Mesothene desperata    | LEMMZ258-10      | 6.56           |
| Lepidoptera | Arctiidae | Rhynchopyga meisteri   | 0.3           | 0.51         | Opharus basalis        | LEMMZ710-11      | 5.96           |
| Lepidoptera | Arctiidae | Sarosa sp. ML01        | 0             | 0            | Dycladia lucetius      | LEMMZ518-11      | 4.67           |
| Lepidoptera | Arctiidae | Saurita sp. JAT01      | 0             | 0            | Arctiinae sp. JAT07    | LEMMZ497-11      | 0              |
| Lepidoptera | Arctiidae | Sciopsycha tropica     | N/A           | N/A          | Leucanopsis leucanina  | LEMMZ1096-12     | 7.39           |
| Lepidoptera | Arctiidae | Stenognatha gentilis   | 0.37          | 0.77         | Barilius acuminata     | LEMMZ1316-12     | 6.55           |
| Lepidoptera | Arctiidae | Theages leucophaea     | 4.15          | 5.93         | Eucereon griseata      | LEMMZ1212-12     | 5.43           |

|             |           |                         |      |      |                           |              |       |
|-------------|-----------|-------------------------|------|------|---------------------------|--------------|-------|
| Lepidoptera | Arctiidae | Tipulodes ima           | N/A  | N/A  | Napata sp. JAT01          | LEMMZ271-10  | 6.18  |
| Lepidoptera | Erebidae  | Agaraea semivittrea     | 6.4  | 9.47 | Pachydota affinis         | LEMMZ1202-12 | 7.4   |
| Lepidoptera | Erebidae  | Agryllis polysemata     | 0    | 0    | Agryllis sp. JAT02        | LEMMZ1295-12 | 0     |
| Lepidoptera | Erebidae  | Agryllis sp. JAT01      | 0.11 | 0.32 | Agryllis sp. JAT09        | LEMMZ647-11  | 6.77  |
| Lepidoptera | Erebidae  | Agryllis sp. JAT02      | 0.14 | 0.31 | Agryllis polysemata       | LEMMZ1298-12 | 0     |
| Lepidoptera | Erebidae  | Agryllis sp. JAT03      | 0.05 | 0.15 | Agryllis sp. JAT04        | LEMMZ391-11  | 3.93  |
| Lepidoptera | Erebidae  | Agryllis sp. JAT04      | 0    | 0    | Agryllis sp. JAT03        | LEMMZ1301-12 | 3.93  |
| Lepidoptera | Erebidae  | Agryllis sp. JAT05      | 0    | 0    | Agryllis sp. JAT02        | LEMMZ1295-12 | 0     |
| Lepidoptera | Erebidae  | Agryllis sp. JAT06      | 0.2  | 0.31 | Agryllis sp. JAT04        | LEMMZ391-11  | 5.25  |
| Lepidoptera | Erebidae  | Agryllis sp. JAT07      | 0.08 | 0.15 | Agryllis sp. JAT08        | LEMMZ1263-12 | 0     |
| Lepidoptera | Erebidae  | Agryllis sp. JAT08      | 3.12 | 7.08 | Agryllis sp. JAT07        | LEMMZ921-11  | 0     |
| Lepidoptera | Erebidae  | Agryllis sp. JAT09      | 0.24 | 0.47 | Agryllis sp. JAT15        | LEMMZ1283-12 | 4.46  |
| Lepidoptera | Erebidae  | Agryllis sp. JAT10      | 0.04 | 0.15 | Agryllis sp. JAT13        | LEMMZ1142-12 | 7.63  |
| Lepidoptera | Erebidae  | Agryllis sp. JAT11      | 1.55 | 1.55 | Agryllis sp. JAT04        | LEMMZ391-11  | 7.57  |
| Lepidoptera | Erebidae  | Agryllis sp. JAT12      | 0.06 | 0.15 | Agryllis sp. JAT11        | LEMMZ874-11  | 7.82  |
| Lepidoptera | Erebidae  | Agryllis sp. JAT13      | 3.15 | 4.58 | Agryllis sp. JAT15        | LEMMZ1300-12 | 0     |
| Lepidoptera | Erebidae  | Agryllis sp. JAT14      | 0    | 0    | Galethalea pica           | LEMMZ733-11  | 5.23  |
| Lepidoptera | Erebidae  | Agryllis sp. JAT15      | 0.2  | 0.31 | Agryllis sp. JAT13        | LEMMZ657-11  | 0     |
| Lepidoptera | Erebidae  | Agryllis sp. ML17       | N/A  | N/A  | Sutonocrea reducta        | LEMMZ452-11  | 10.84 |
| Lepidoptera | Erebidae  | Amoxia corata           | 0.31 | 0.46 | Sutonocrea reducta        | LEMMZ452-11  | 8.24  |
| Lepidoptera | Erebidae  | Amoxia hebe             | 0.2  | 0.31 | Symphlebia lophocampoides | LEMMZ314-10  | 7.79  |
| Lepidoptera | Erebidae  | Amoxia sp. ML01         | N/A  | N/A  | Elysius superba           | LEMMZ770-11  | 8.79  |
| Lepidoptera | Erebidae  | Ammalo helops           | 0.12 | 0.31 | Baritis acuminata         | LEMMZ835-11  | 6.72  |
| Lepidoptera | Erebidae  | Aphyle abdominalis      | 0.2  | 0.31 | Pelochyta sp. JAT01       | LEMMZ459-11  | 7.39  |
| Lepidoptera | Erebidae  | Apistosis judas         | N/A  | N/A  | Agryllis sp. JAT09        | LEMMZ647-11  | 5.88  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT01     | 0.54 | 1.08 | Dinia sp. JAT01           | LEMMZ504-11  | 6.89  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT08     | N/A  | N/A  | Galethalea pica           | LEMMZ060-10  | 6.8   |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT09     | 0.31 | 0.31 | Dycladia lucetius         | LEMMZ519-11  | 6.06  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT16     | 0.31 | 0.31 | Pachydota sp. JAT01       | LEMMZ1308-12 | 2.65  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT17     | N/A  | N/A  | Pelochyta sp. JAT01       | LEMMZ1016-11 | 5.91  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT02     | 0.15 | 0.15 | Galethalea pica           | LEMMZ733-11  | 5.9   |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT03     | 0    | 0    | Eucereon sp. JAT03        | LEMMZ1161-12 | 0.46  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT04     | N/A  | N/A  | Galethalea pica           | LEMMZ733-11  | 7.23  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT05     | N/A  | N/A  | Arctiidae sp. JAT21       | LEMMZ1108-12 | 6.72  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT06     | 0    | 0    | Galethalea pica           | LEMMZ733-11  | 6.39  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT07     | N/A  | N/A  | Saurita sp. JAT01         | LEMMZ255-10  | 0     |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT10     | N/A  | N/A  | Dycladia lucetius         | LEMMZ518-11  | 5.42  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT11     | N/A  | N/A  | Dycladia lucetius         | LEMMZ518-11  | 7.22  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT12     | 0.1  | 0.15 | Dycladia lucetius         | LEMMZ519-11  | 5.06  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT14     | N/A  | N/A  | Cosmosoma leuconotus      | LEMMZ502-11  | 4.59  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT15     | 0.41 | 0.62 | Dycladia lucetius         | LEMMZ518-11  | 3.61  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT18     | 0    | 0    | Leucanopsis sp. JAT08     | LEMMZ1086-12 | 0     |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT20     | N/A  | N/A  | Delphyre flaviceps        | LEMMZ267-10  | 6.22  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT21     | N/A  | N/A  | Trichromia sp. JAT04      | LEMMZ588-11  | 1.87  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT22     | 0    | 0    | Symphlebia lophocampoides | LEMMZ314-10  | 7.46  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT23     | 0.56 | 1.24 | Arctiidae sp. JAT28       | LEMMZ1150-12 | 6.55  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT24     | 0    | 0    | Leucanopsis sp. JAT03     | LEMMZ945-11  | 4.42  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT25     | N/A  | N/A  | Leucanopsis sp. JAT04     | LEMMZ891-11  | 0     |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT26     | 0    | 0    | Arctiidae sp. JAT33       | LEMMZ1256-12 | 4.78  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT27     | 4.5  | 9.15 | Leucanopsis sp. JAT06     | LEMMZ554-11  | 2.65  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT28     | 2.82 | 2.82 | Leucanopsis sp. JAT03     | LEMMZ550-11  | 3.29  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT29     | 0    | 0    | Melese sp. JAT07          | LEMMZ998-11  | 8.78  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT30     | N/A  | N/A  | Symphlebia perflua        | LEMMZ396-11  | 0     |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT31     | N/A  | N/A  | Machadoia xanthosticta    | LEMMZ399-11  | 4.92  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT32     | 4.6  | 9.47 | Leucanopsis sp. JAT02     | LEMMZ1015-11 | 0     |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT33     | 0    | 0    | Arctiidae sp. JAT26       | LEMMZ1244-12 | 4.78  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT34     | 1.87 | 1.87 | Arctiidae sp. JAT32       | LEMMZ1236-12 | 0.15  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT35     | 0    | 0    | Bertholdia soror          | LEMMZ384-11  | 6.9   |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT37     | 0    | 0    | Delphyre flaviceps        | LEMMZ267-10  | 6.77  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT38     | 0.8  | 1.4  | Hyperbaeophis sp. ML01    | LEMMZ1129-12 | 6.38  |
| Lepidoptera | Erebidae  | Arctiidae sp. JAT39     | 0.52 | 0.92 | Dinia sp. JAT01           | LEMMZ504-11  | 6.73  |
| Lepidoptera | Erebidae  | Arhabdosia sp. ML01     | 0.83 | 1.24 | Talara sp. ML01           | LEMMZ1279-12 | 4.43  |
| Lepidoptera | Erebidae  | Aristodaema hanga       | 0.54 | 1.08 | Mirandisca harpalyce      | LEMMZ757-11  | 6.41  |
| Lepidoptera | Erebidae  | Baritis acuminata       | 1.45 | 2.18 | Pachydota affinis         | LEMMZ688-11  | 3.76  |
| Lepidoptera | Erebidae  | Baritis sp. ML01        | 2.54 | 5.06 | Pelochyta sp. JAT01       | LEMMZ837-11  | 5.89  |
| Lepidoptera | Erebidae  | Bernathonomus piperita  | 0    | 0    | Arctiidae sp. JAT32       | LEMMZ1241-12 | 4.41  |
| Lepidoptera | Erebidae  | Bertholdia pseudofumida | 0.51 | 0.77 | Bertholdia soror          | LEMMZ384-11  | 4.75  |
| Lepidoptera | Erebidae  | Bertholdia soror        | 0.93 | 1.24 | Melese sp. JAT09          | LEMMZ989-11  | 4.58  |
| Lepidoptera | Erebidae  | Carales astur           | 0.1  | 0.15 | Arctiidae sp. JAT31       | LEMMZ1251-12 | 5.89  |
| Lepidoptera | Erebidae  | Carathis byblis         | 0    | 0    | Sutonocrea reducta        | LEMMZ452-11  | 8.27  |
| Lepidoptera | Erebidae  | Castrica phalaenoides   | 0.2  | 0.31 | Melese sp. JAT07          | LEMMZ435-11  | 8.41  |
| Lepidoptera | Erebidae  | Cissura decora          | 0.12 | 0.31 | Bertholdia soror          | LEMMZ384-11  | 7.06  |
| Lepidoptera | Erebidae  | Clemensia marmorata     | 0    | 0    | Pronola sp. ML01          | LEMMZ938-11  | 6.73  |
| Lepidoptera | Erebidae  | Cloesia sp. ML01        | 0.09 | 0.31 | Illice ditrigona          | LEMMZ934-11  | 7.05  |
| Lepidoptera | Erebidae  | Correbidia elegans      | 2.27 | 4.3  | Correbidia sp. JAT01      | LEMMZ844-11  | 0     |
| Lepidoptera | Erebidae  | Correbidia lycoides     | 0.27 | 0.46 | Eucereon quadricolor      | LEMMZ305-10  | 8.93  |
| Lepidoptera | Erebidae  | Correbidia sp. JAT01    | 0.1  | 0.15 | Correbidia elegans        | LEMMZ700-11  | 0     |

|             |          |                          |       |       |                          |              |       |
|-------------|----------|--------------------------|-------|-------|--------------------------|--------------|-------|
| Lepidoptera | Erebidae | Correbidia sp. JAT02     | N/A   | N/A   | Eucereon quadricolor     | LEMMZ305-10  | 6.55  |
| Lepidoptera | Erebidae | Cosmosoma auge           | 3.22  | 4.76  | Dycladia lucetius        | LEMMZ518-11  | 4.75  |
| Lepidoptera | Erebidae | Cosmosoma centrale       | 0.08  | 0.15  | Mesothera desperata      | LEMMZ258-10  | 4.42  |
| Lepidoptera | Erebidae | Cosmosoma durca          | 0.2   | 0.31  | Cosmosoma elegans        | LEMMZ787-11  | 4.42  |
| Lepidoptera | Erebidae | Cosmosoma elegans        | 0.15  | 0.31  | Cosmosoma sp. JAT02      | LEMMZ493-11  | 2.81  |
| Lepidoptera | Erebidae | Cosmosoma klagesi        | 0     | 0     | Mirandisca harpalyce     | LEMMZ757-11  | 2.49  |
| Lepidoptera | Erebidae | Cosmosoma leuconoton     | 0     | 0     | Cosmosoma plutona        | LEMMZ505-11  | 3.13  |
| Lepidoptera | Erebidae | Cosmosoma plutona        | 0.15  | 0.15  | Cosmosoma leuconoton     | LEMMZ502-11  | 3.13  |
| Lepidoptera | Erebidae | Cosmosoma sp. JAT01      | 0     | 0     | Cosmosoma elegans        | LEMMZ787-11  | 2.83  |
| Lepidoptera | Erebidae | Cosmosoma sp. JAT02      | 0     | 0     | Cosmosoma elegans        | LEMMZ393-11  | 2.81  |
| Lepidoptera | Erebidae | Cosmosoma sp. JAT03      | N/A   | N/A   | Dycladia lucetius        | LEMMZ518-11  | 5.23  |
| Lepidoptera | Erebidae | Cosmosoma sp. JAT04      | 0     | 0     | Dycladia lucetius        | LEMMZ518-11  | 4.43  |
| Lepidoptera | Erebidae | Cosmosoma teuthras       | 1.67  | 2.5   | Dycladia lucetius        | LEMMZ518-11  | 4.74  |
| Lepidoptera | Erebidae | Cratoplastis catherinae  | 0     | 0     | Viviennea morma          | LEMMZ1104-12 | 5.57  |
| Lepidoptera | Erebidae | Ctenucha jonesi          | N/A   | N/A   | Galethalea pica          | LEMMZ733-11  | 5.58  |
| Lepidoptera | Erebidae | Delphyre flaviceps       | 0.2   | 0.31  | Aglyta sp. JAT14         | LEMMZ1082-12 | 5.73  |
| Lepidoptera | Erebidae | Delphyre hebes           | N/A   | N/A   | Galethalea pica          | LEMMZ733-11  | 8.77  |
| Lepidoptera | Erebidae | Delphyre pyroperas       | N/A   | N/A   | Galethalea pica          | LEMMZ733-11  | 6.72  |
| Lepidoptera | Erebidae | Delphyre sp. ML01        | 1.12  | 1.87  | Baritius acuminata       | LEMMZ297-10  | 4.57  |
| Lepidoptera | Erebidae | Demolis albicostata      | N/A   | N/A   | Bertholdia soror         | LEMMZ384-11  | 8.93  |
| Lepidoptera | Erebidae | Dysschema amphisa        | 1.82  | 3.15  | Dysschema sp. JAT01      | LEMMZ368-10  | 3.95  |
| Lepidoptera | Erebidae | Dysschema fantasma       | 0.1   | 0.15  | Dysschema sp. JAT01      | LEMMZ368-10  | 4.12  |
| Lepidoptera | Erebidae | Dysschema hilarina       | 4.73  | 4.73  | Dysschema neda           | LEMMZ602-11  | 6.63  |
| Lepidoptera | Erebidae | Dysschema lucifer        | 0.34  | 0.62  | Dysschema sp. JAT01      | LEMMZ368-10  | 5.13  |
| Lepidoptera | Erebidae | Dysschema neda           | N/A   | N/A   | Dysschema hilarina       | LEMMZ779-11  | 6.63  |
| Lepidoptera | Erebidae | Dysschema sacrifica      | N/A   | N/A   | Dysschema fantasma       | LEMMZ799-11  | 7.81  |
| Lepidoptera | Erebidae | Dysschema sp. JAT01      | 0.32  | 0.62  | Dysschema amphisa        | LEMMZ402-11  | 3.95  |
| Lepidoptera | Erebidae | Dysschema subapicalis    | N/A   | N/A   | Dysschema neda           | LEMMZ602-11  | 7.13  |
| Lepidoptera | Erebidae | Echeta divisa            | 0.31  | 0.31  | Rhipha subflammas        | LEMMZ681-11  | 8.29  |
| Lepidoptera | Erebidae | Echeta sp. JAT01         | 0     | 0     | Baritius sp. ML01        | LEMMZ627-11  | 10.94 |
| Lepidoptera | Erebidae | Elysia cingulata         | 0.15  | 0.15  | Phaegoptera chorima      | LEMMZ1193-12 | 4.74  |
| Lepidoptera | Erebidae | Elysia pyrosticta        | 3.58  | 6.07  | Phaegoptera chorima      | LEMMZ1193-12 | 4.41  |
| Lepidoptera | Erebidae | Elysia superba           | 2.66  | 2.66  | Machadoia xanthosticta   | LEMMZ543-11  | 6.47  |
| Lepidoptera | Erebidae | Episcepsis endodasia     | 0.31  | 0.62  | Delphyre flaviceps       | LEMMZ267-10  | 6.9   |
| Lepidoptera | Erebidae | Episcepsis venata        | 0.2   | 0.31  | Galethalea pica          | LEMMZ060-10  | 5.58  |
| Lepidoptera | Erebidae | Erruca cardinale         | 0.2   | 0.31  | Dycladia lucetius        | LEMMZ518-11  | 4.75  |
| Lepidoptera | Erebidae | Erruca deyrollei         | 0     | 0     | Dycladia lucetius        | LEMMZ518-11  | 5.93  |
| Lepidoptera | Erebidae | Erruca sanguipuncta      | 0.31  | 0.62  | Dycladia lucetius        | LEMMZ518-11  | 4.26  |
| Lepidoptera | Erebidae | Eucereon apicalis        | 0.12  | 0.32  | Aglyta sp. JAT14         | LEMMZ1082-12 | 6.74  |
| Lepidoptera | Erebidae | Eucereon chalcodon       | 0.83  | 1.24  | Euceriodes wernickei     | LEMMZ1229-12 | 6.07  |
| Lepidoptera | Erebidae | Eucereon discolor        | 0.15  | 0.31  | Galethalea pica          | LEMMZ806-11  | 8.49  |
| Lepidoptera | Erebidae | Eucereon griseata        | 0.21  | 0.62  | Theages leucophaea       | LEMMZ051-10  | 5.43  |
| Lepidoptera | Erebidae | Eucereon quadricolor     | 0     | 0     | Aglyta sp. JAT14         | LEMMZ1082-12 | 6.05  |
| Lepidoptera | Erebidae | Eucereon rosa            | 1.67  | 4.94  | Galethalea pica          | LEMMZ733-11  | 5.72  |
| Lepidoptera | Erebidae | Eucereon setosum         | 0     | 0     | Galethalea pica          | LEMMZ060-10  | 3.24  |
| Lepidoptera | Erebidae | Eucereon sp. JAT01       | 0.1   | 0.15  | Eucereon chalcodon       | LEMMZ810-11  | 6.73  |
| Lepidoptera | Erebidae | Eucereon sp. JAT02       | 12.49 | 12.49 | Trichromia sp. JAT06     | LEMMZ594-11  | 0     |
| Lepidoptera | Erebidae | Eucereon sp. JAT03       | 0.15  | 0.15  | Arctiinae sp. JAT03      | LEMMZ1163-12 | 0.46  |
| Lepidoptera | Erebidae | Eucereon sp. JAT04       | 0.1   | 0.15  | Aclytia sp. JAT01        | LEMMZ807-11  | 0     |
| Lepidoptera | Erebidae | Eucereon tarona          | 0     | 0     | Galethalea pica          | LEMMZ060-10  | 7.66  |
| Lepidoptera | Erebidae | Euceriodes wernickei     | 6.66  | 9.13  | Eucereon chalcodon       | LEMMZ810-11  | 6.07  |
| Lepidoptera | Erebidae | Eupseudosoma involuta    | 7.27  | 10.9  | Hyperandra appendiculata | LEMMZ663-11  | 6.89  |
| Lepidoptera | Erebidae | Euthyone purpurea        | N/A   | N/A   | Tricypha sp. JAT01       | LEMMZ709-11  | 10.15 |
| Lepidoptera | Erebidae | Galethalea pica          | 0.21  | 0.32  | Eucereon setosum         | LEMMZ531-11  | 3.24  |
| Lepidoptera | Erebidae | Grapheia paramarmorea    | 0.77  | 0.77  | Baritius sp. ML01        | LEMMZ627-11  | 6.91  |
| Lepidoptera | Erebidae | Haemanota bicolor        | N/A   | N/A   | Trichromia sp. JAT05     | LEMMZ831-11  | 8.41  |
| Lepidoptera | Erebidae | Heterodontia haematica   | 0.05  | 0.15  | Dycladia lucetius        | LEMMZ518-11  | 6.56  |
| Lepidoptera | Erebidae | Holophaea erharda        | 0     | 0     | Ichoria tricincta        | LEMMZ496-11  | 7.41  |
| Lepidoptera | Erebidae | Hyperandra appendiculata | 0     | 0     | Eupseudosoma involuta    | LEMMZ354-10  | 6.89  |
| Lepidoptera | Erebidae | Hypercompe sp. JAT01     | 0     | 0     | Machadoia xanthosticta   | LEMMZ731-11  | 9.04  |
| Lepidoptera | Erebidae | Hypermaepha sp. ML01     | 0.07  | 0.46  | Lycomorphodes sp. ML01   | LEMMZ1311-12 | 6.23  |
| Lepidoptera | Erebidae | Hypidalia enervis        | 0     | 0     | Eupseudosoma involuta    | LEMMZ354-10  | 7.9   |
| Lepidoptera | Erebidae | Idalus agastus           | 7.27  | 10.11 | Idalus sp. JAT01         | LEMMZ1186-12 | 0     |
| Lepidoptera | Erebidae | Idalus lineosus          | 5.24  | 10.07 | Ormetica rothschildi     | LEMMZ1223-12 | 8.76  |
| Lepidoptera | Erebidae | Idalus sp. JAT01         | 3.2   | 6.63  | Idalus agastus           | LEMMZ690-11  | 0     |
| Lepidoptera | Erebidae | Illice brunnea           | 4.88  | 8.26  | Illice sp. ML01          | LEMMZ925-11  | 0     |
| Lepidoptera | Erebidae | Illice cryptopygra       | 0.16  | 0.16  | Baritius acuminata       | LEMMZ297-10  | 6.26  |
| Lepidoptera | Erebidae | Illice ditrigona         | 0.22  | 0.49  | Illice sp. ML05          | LEMMZ933-11  | 6.38  |
| Lepidoptera | Erebidae | Illice endoxantha        | 0.17  | 0.46  | Illice sp. ML04          | LEMMZ860-11  | 3.93  |
| Lepidoptera | Erebidae | Illice sp. ML01          | 0.41  | 0.62  | Illice brunnea           | LEMMZ920-11  | 0     |
| Lepidoptera | Erebidae | Illice sp. ML02          | N/A   | N/A   | Illice sp. ML03          | LEMMZ861-11  | 10.68 |
| Lepidoptera | Erebidae | Illice sp. ML03          | N/A   | N/A   | Baritius acuminata       | LEMMZ297-10  | 9.62  |
| Lepidoptera | Erebidae | Illice sp. ML04          | 2.67  | 3.96  | Illice endoxantha        | LEMMZ941-11  | 3.93  |
| Lepidoptera | Erebidae | Illice sp. ML05          | 0     | 0     | Illice ditrigona         | LEMMZ934-11  | 6.38  |
| Lepidoptera | Erebidae | Ischnocampa lugubris     | 2.18  | 4.11  | Phaegoptera chorima      | LEMMZ1193-12 | 6.23  |
| Lepidoptera | Erebidae | Ischnognatha leucopera   | 0     | 0     | Rhynchopyga meisteri     | LEMMZ524-11  | 8.57  |

|             |          |                                |      |       |                        |              |       |
|-------------|----------|--------------------------------|------|-------|------------------------|--------------|-------|
| Lepidoptera | Erebidae | Isia alcumena                  | 0.2  | 0.31  | Illice sp. ML05        | LEMMZ933-11  | 9.46  |
| Lepidoptera | Erebidae | Lepidokirbyia vittipes         | 0.1  | 0.15  | Ormetica iheringi      | LEMMZ1201-12 | 8.42  |
| Lepidoptera | Erebidae | Lepidozikania sp. JAT01        | 0.23 | 0.46  | Aglyia sp. JAT14       | LEMMZ1082-12 | 6.41  |
| Lepidoptera | Erebidae | Leucanopsis coniota            | 0.2  | 0.31  | Arctiinae sp. JAT32    | LEMMZ1241-12 | 3.95  |
| Lepidoptera | Erebidae | Leucanopsis leucanina          | 1.55 | 1.55  | Leucanopsis sp. JAT07  | LEMMZ1085-12 | 4.77  |
| Lepidoptera | Erebidae | Leucanopsis mandus             | 0    | 0     | Arctiinae sp. JAT32    | LEMMZ1241-12 | 3.93  |
| Lepidoptera | Erebidae | Leucanopsis oruba              | 0    | 0     | Arctiinae sp. JAT32    | LEMMZ1241-12 | 3.31  |
| Lepidoptera | Erebidae | Leucanopsis sp. JAT01          | 0.09 | 0.15  | Arctiinae sp. JAT32    | LEMMZ1241-12 | 4.75  |
| Lepidoptera | Erebidae | Leucanopsis sp. JAT02          | N/A  | N/A   | Arctiinae sp. JAT32    | LEMMZ1236-12 | 0     |
| Lepidoptera | Erebidae | Leucanopsis sp. JAT03          | 0.3  | 0.62  | Arctiinae sp. JAT28    | LEMMZ1150-12 | 3.29  |
| Lepidoptera | Erebidae | Leucanopsis sp. JAT04          | 5.99 | 12.74 | Arctiinae sp. JAT25    | LEMMZ1148-12 | 0     |
| Lepidoptera | Erebidae | Leucanopsis sp. JAT05          | 0.2  | 0.31  | Barilius acuminata     | LEMMZ297-10  | 5.23  |
| Lepidoptera | Erebidae | Leucanopsis sp. JAT06          | N/A  | N/A   | Leucanopsis sp. JAT04  | LEMMZ876-11  | 0     |
| Lepidoptera | Erebidae | Leucanopsis sp. JAT07          | 0    | 0     | Arctiinae sp. JAT27    | LEMMZ1262-12 | 4.43  |
| Lepidoptera | Erebidae | Leucanopsis sp. JAT08          | 1.08 | 1.08  | Arctiinae sp. JAT18    | LEMMZ545-11  | 0     |
| Lepidoptera | Erebidae | Lophocampa arpi                | 0.15 | 0.15  | Opharus notata         | LEMMZ1089-12 | 4.27  |
| Lepidoptera | Erebidae | Lophocampa sp. JAT01           | 2.14 | 4.28  | Lophocampa texta       | LEMMZ1259-12 | 3.29  |
| Lepidoptera | Erebidae | Lophocampa sp. JAT02           | 3.54 | 5.57  | Lophocampa sp. JAT01   | LEMMZ949-11  | 4.61  |
| Lepidoptera | Erebidae | Lophocampa texta               | 1.32 | 3.6   | Lophocampa sp. JAT01   | LEMMZ949-11  | 3.29  |
| Lepidoptera | Erebidae | Lycomorphodes sp. ML01         | 0.72 | 0.93  | Lycomorphodes strigosa | LEMMZ1139-12 | 0.15  |
| Lepidoptera | Erebidae | Lycomorphodes strigosa         | 0.93 | 0.93  | Lycomorphodes sp. ML01 | LEMMZ1311-12 | 0.15  |
| Lepidoptera | Erebidae | Machadoia xanthosticta         | 3.83 | 7.36  | Phaegoptera chorima    | LEMMZ1193-12 | 4.02  |
| Lepidoptera | Erebidae | Macrocneme sp. JAT01           | 2.79 | 5.48  | Galethalea pica        | LEMMZ733-11  | 8.08  |
| Lepidoptera | Erebidae | Mazaeras francki               | 0.18 | 0.46  | Opharus notata         | LEMMZ1089-12 | 5.73  |
| Lepidoptera | Erebidae | Melese castrena                | 2.45 | 5.1   | Melese sp. JAT08       | LEMMZ979-11  | 0     |
| Lepidoptera | Erebidae | Melese chozeba                 | 0.31 | 1.4   | Bertholdia soror       | LEMMZ384-11  | 5.23  |
| Lepidoptera | Erebidae | Melese incertus                | 5.72 | 9.65  | Arctiinae sp. JAT32    | LEMMZ957-11  | 0     |
| Lepidoptera | Erebidae | Melese sp. JAT01               | 0.34 | 1.47  | Melese sp. JAT03       | LEMMZ855-11  | 0     |
| Lepidoptera | Erebidae | Melese sp. JAT02               | 0.34 | 0.77  | Melese sp. JAT09       | LEMMZ988-11  | 6.34  |
| Lepidoptera | Erebidae | Melese sp. JAT03               | 0.43 | 0.82  | Melese sp. JAT01       | LEMMZ977-11  | 0     |
| Lepidoptera | Erebidae | Melese sp. JAT04               | 0.15 | 0.31  | Melese sp. JAT11       | LEMMZ1238-12 | 0     |
| Lepidoptera | Erebidae | Melese sp. JAT05               | 0.26 | 0.77  | Melese sp. JAT07       | LEMMZ994-11  | 7.9   |
| Lepidoptera | Erebidae | Melese sp. JAT06               | 0.04 | 0.15  | Melese incertus        | LEMMZ697-11  | 0     |
| Lepidoptera | Erebidae | Melese sp. JAT07               | 0.43 | 0.93  | Melese sp. JAT10       | LEMMZ991-11  | 0     |
| Lepidoptera | Erebidae | Melese sp. JAT08               | 0    | 0     | Melese castrena        | LEMMZ404-11  | 0     |
| Lepidoptera | Erebidae | Melese sp. JAT09               | 0.38 | 0.8   | Bertholdia soror       | LEMMZ384-11  | 4.58  |
| Lepidoptera | Erebidae | Melese sp. JAT10               | 2.22 | 4.11  | Melese sp. JAT07       | LEMMZ1001-11 | 0     |
| Lepidoptera | Erebidae | Melese sp. JAT11               | N/A  | N/A   | Melese sp. JAT04       | LEMMZ959-11  | 0     |
| Lepidoptera | Erebidae | Melese sp. JAT12               | N/A  | N/A   | Melese incertus        | LEMMZ952-11  | 0     |
| Lepidoptera | Erebidae | Metalobosia diaxantha          | 3.71 | 6.91  | Talara sp. ML01        | LEMMZ1279-12 | 8.24  |
| Lepidoptera | Erebidae | Mirandisca harpalyce           | 0.08 | 0.15  | Cosmosoma klagesi      | LEMMZ046-10  | 2.49  |
| Lepidoptera | Erebidae | Neidalia dulcicula             | N/A  | N/A   | Leucanopsis leucanina  | LEMMZ1257-12 | 10.7  |
| Lepidoptera | Erebidae | Neonerita dorsipuncta          | 0.1  | 0.15  | Lepidokirbyia vittipes | LEMMZ1093-12 | 10.88 |
| Lepidoptera | Erebidae | Neotrichura nigripes           | 0.08 | 0.15  | Melese sp. JAT09       | LEMMZ988-11  | 6.32  |
| Lepidoptera | Erebidae | Nodozana coresa                | 6.75 | 9.98  | Melese castrena        | LEMMZ624-11  | 7.55  |
| Lepidoptera | Erebidae | Ochrodota pronapides           | 0.07 | 0.16  | Barilius acuminata     | LEMMZ297-10  | 5.39  |
| Lepidoptera | Erebidae | Opharus basalis                | 0    | 0     | Pachydota affinis      | LEMMZ688-11  | 5.06  |
| Lepidoptera | Erebidae | Opharus brasiliensis           | 0    | 0     | Phaegoptera chorima    | LEMMZ1193-12 | 6.05  |
| Lepidoptera | Erebidae | Opharus notata                 | 0.1  | 0.15  | Lophocampa arpi        | LEMMZ736-11  | 4.27  |
| Lepidoptera | Erebidae | Opharus procroides             | 0    | 0     | Opharus brasiliensis   | LEMMZ467-11  | 6.95  |
| Lepidoptera | Erebidae | Opharus rema                   | 0    | 0     | Arctiidae sp. JAT16    | LEMMZ536-11  | 7.22  |
| Lepidoptera | Erebidae | Ormetica iheringi              | 0    | 0     | Ormetica rothschildi   | LEMMZ1223-12 | 4.27  |
| Lepidoptera | Erebidae | Ormetica rothschildi           | 0    | 0     | Ormetica iheringi      | LEMMZ1201-12 | 4.27  |
| Lepidoptera | Erebidae | Pachydota affinis              | 3.8  | 5.89  | Barilius acuminata     | LEMMZ297-10  | 3.76  |
| Lepidoptera | Erebidae | Pachydota sp. JAT01            | N/A  | N/A   | Phaegoptera fusca      | LEMMZ059-10  | 0.46  |
| Lepidoptera | Erebidae | Paracles fusca                 | 5.27 | 8.75  | Paracles sp. JAT04     | LEMMZ1314-12 | 6.12  |
| Lepidoptera | Erebidae | Paracles sp. JAT01             | N/A  | N/A   | Paracles sp. JAT03     | LEMMZ1159-12 | 6.58  |
| Lepidoptera | Erebidae | Paracles sp. JAT02             | 0    | 0     | Paracles sp. JAT01     | LEMMZ568-11  | 7.25  |
| Lepidoptera | Erebidae | Paracles sp. JAT03             | N/A  | N/A   | Paracles sp. JAT01     | LEMMZ568-11  | 6.58  |
| Lepidoptera | Erebidae | Paracles sp. JAT04             | N/A  | N/A   | Paracles fusca         | LEMMZ1315-12 | 6.12  |
| Lepidoptera | Erebidae | Paracles variegata             | 0    | 0     | Paracles sp. JAT03     | LEMMZ1159-12 | 8.29  |
| Lepidoptera | Erebidae | Pareuchaetes sp. ML01          | 0    | 0     | Pelochyta sp. JAT01    | LEMMZ459-11  | 7.73  |
| Lepidoptera | Erebidae | Pelochyta cinerea              | 2.7  | 5.4   | Barilius acuminata     | LEMMZ297-10  | 4.58  |
| Lepidoptera | Erebidae | Pelochyta sp. JAT01            | 0.31 | 0.46  | Arctiinae sp. JAT28    | LEMMZ1150-12 | 4.25  |
| Lepidoptera | Erebidae | Phaegoptera chorima            | 0.22 | 0.46  | Arctiidae sp. JAT16    | LEMMZ536-11  | 2.66  |
| Lepidoptera | Erebidae | Phaegoptera fusca              | 1.68 | 3.45  | Pachydota sp. JAT01    | LEMMZ1308-12 | 0.46  |
| Lepidoptera | Erebidae | Phaegoptera histrionica        | 0.37 | 0.62  | Pachydota sp. JAT01    | LEMMZ1308-12 | 2.34  |
| Lepidoptera | Erebidae | Phylorox affinis               | 0.15 | 0.15  | Galethalea pica        | LEMMZ733-11  | 6.76  |
| Lepidoptera | Erebidae | Phoenicoprocta haemorrhoidalis | 0    | 0     | Sychesia dryas         | LEMMZ1221-12 | 8.58  |
| Lepidoptera | Erebidae | Pollopastea indistincta        | 4.91 | 11.35 | Galethalea pica        | LEMMZ806-11  | 6.9   |
| Lepidoptera | Erebidae | Praepiella sesapina            | N/A  | N/A   | Pelochyta sp. JAT01    | LEMMZ837-11  | 9.27  |
| Lepidoptera | Erebidae | Pronola sp. ML01               | 0.28 | 0.46  | Clemensia marmorata    | LEMMZ932-11  | 6.73  |
| Lepidoptera | Erebidae | Pseudosphex rubripalpus        | 0    | 0     | Barilius acuminata     | LEMMZ297-10  | 8.6   |
| Lepidoptera | Erebidae | Psilopleura sanguipuncta       | 0.31 | 0.61  | Dycladia lucetius      | LEMMZ518-11  | 4.09  |
| Lepidoptera | Erebidae | Psychopasma erosa              | N/A  | N/A   | Phaegoptera chorima    | LEMMZ1193-12 | 5.07  |
| Lepidoptera | Erebidae | Rhabdatomis sp. ML01           | 0    | 0     | Lophocampa sp. JAT01   | LEMMZ949-11  | 8.45  |
| Lepidoptera | Erebidae | Rhipha flavithorax             | 0    | 0     | Ormetica rothschildi   | LEMMZ1223-12 | 6.22  |

**Appendix 4III.** intra and interspecific pairwise distances of the species revealed by DNA barcoding.

| Species   | Numbe of sequences | Mean Intra-sp | Max Intra-sp | Nearest species           | Distance to Nearest species |
|---|--------------------|---------------|--------------|---------------------------|-----------------------------|
| Aclytia jonesi+Aclytia heber                          | 7                  | 0.23          | 0.6          | Aclytia jonesi            | 5.9                         |
| Aclytia jonesiMMZ01                                   | 1                  | 0             | 0            | Agylla sp. JAT14          | 5.6                         |
| Aclytia sp. JAT01+Aclytia sp. JAT02+Eucereonsp. JAT04 | 9                  | 0.05          | 0.2          | Epidesma ursula           | 6.3                         |
| Aclytia terra   | 5                  | 1.12          | 1.87         | Aclytia heber             | 6.58                        |
| Agaraea semivitreaMMZ01                               | 2                  | 0.6           | 0.6          | Pachydota affinisMMZ03    | 6.7                         |
| Agaraea semivitreaMMZ02                               | 1                  | 0             | 0            | Phaegoptera fusca         | 9.3                         |
| Agylla sp. JAT01                                      | 9                  | 0.11          | 0.32         | Agylla sp. JAT09          | 6.77                        |
| Agylla sp. JAT02+Agylla sp. JAT05+Agylla polysemata   | 18                 | 0.04          | 0.2          | Agylla sp. JAT15          | 4.2                         |
| Agylla sp. JAT03                                      | 6                  | 0.05          | 0.15         | Agylla sp. JAT04          | 3.93                        |
| Agylla sp. JAT04                                      | 7                  | 0             | 0            | Agylla sp. JAT03          | 3.93                        |
| Agylla sp. JAT06                                      | 7                  | 0.2           | 0.31         | Agylla sp. JAT04          | 5.25                        |
| Agylla sp. JAT08+Agylla sp. JAT07                     | 12                 | 0.18          | 0.4          | Agylla sp. JAT15          | 5.4                         |
| Agylla sp. JAT08MMZ01                                 | 3                  | 0             | 0            | Agylla sp. JAT13          | 3.6                         |
| Agylla sp. JAT09                                      | 9                  | 0.24          | 0.47         | Agylla sp. JAT15          | 4.46                        |
| Agylla sp. JAT10                                      | 8                  | 0.04          | 0.15         | Agylla sp. JAT13          | 7.63                        |
| Agylla sp. JAT11                                      | 2                  | 1.55          | 1.55         | Agylla sp. JAT04          | 7.57                        |
| Agylla sp. JAT12                                      | 5                  | 0.06          | 0.15         | Agylla sp. JAT11          | 7.82                        |
| Agylla sp. JAT13                                      | 1                  | 0             | 0            | Agylla sp. JAT08          | 3.6                         |
| Agylla sp. JAT13+Agylla sp. JAT15                     | 5                  | 0.24          | 0.6          | Agylla sp. JAT02          | 4                           |
| Agylla sp. JAT14                                      | 3                  | 0             | 0            | Galethalea pica           | 5.23                        |
| Agylla sp. ML17                                       | 1                  | N/A           | N/A          | Sutonocrea reducta        | 10.84                       |
| Agyrta albisparsa                                     | 5                  | 0.09          | 0.15         | Galethalea pica           | 6.56                        |
| Amaxia corata   | 4                  | 0.31          | 0.46         | Sutonocrea reducta        | 8.24                        |
| Amaxia hebe   | 3                  | 0.2           | 0.31         | Symphlebia lophocampoides | 7.79                        |
| Amaxia sp. ML01                                       | 1                  | N/A           | N/A          | Elysium superba           | 8.79                        |
| Ammalo helops   | 5                  | 0.12          | 0.31         | Baritius acuminata        | 6.72                        |
| Aphyle abdominalis                                    | 3                  | 0.2           | 0.31         | Pelochyta sp. JAT01       | 7.39                        |
| Apistosia judas                                       | 1                  | N/A           | N/A          | Agylla sp. JAT09          | 5.88                        |

|   |   |      |      |                           |      |
|---|---|------|------|---------------------------|------|
| Arctiinae sp. 27 MMZ01  | 3 | 0.13 | 0.2  | Leucanopsis sp. JAT06     | 2    |
| Arctiinae sp. 27 MMZ02  | 7 | 0    | 0    | Leucanopsis sp. JAT07     | 3.6  |
| Arctiinae sp. JAT01   | 4 | 0.54 | 1.08 | Dinia sp. JAT01           | 6.89 |
| Arctiinae sp. JAT02   | 2 | 0.15 | 0.15 | Galethalea pica           | 5.9  |
| Arctiinae sp. JAT04   | 1 | N/A  | N/A  | Galethalea pica           | 7.23 |
| Arctiinae sp. JAT05   | 1 | N/A  | N/A  | Arctiinae sp. JAT21       | 6.72 |
| Arctiinae sp. JAT06   | 3 | 0    | 0    | Galethalea pica           | 6.39 |
| Arctiinae sp. JAT08   | 1 | N/A  | N/A  | Galethalea pica           | 6.8  |
| Arctiinae sp. JAT09   | 3 | 0.31 | 0.31 | Dycladia lucetius         | 6.06 |
| Arctiinae sp. JAT10   | 1 | N/A  | N/A  | Dycladia lucetius         | 5.42 |
| Arctiinae sp. JAT11   | 1 | N/A  | N/A  | Dycladia lucetius         | 7.22 |
| Arctiinae sp. JAT12   | 3 | 0.1  | 0.15 | Dycladia lucetius         | 5.06 |
| Arctiinae sp. JAT14   | 1 | N/A  | N/A  | Cosmosoma leuconoton      | 4.59 |
| Arctiinae sp. JAT15   | 3 | 0.41 | 0.62 | Dycladia lucetius         | 3.61 |
| Arctiinae sp. JAT16   | 2 | 0.31 | 0.31 | Pachydota sp. JAT01       | 2.65 |
| Arctiinae sp. JAT17   | 1 | N/A  | N/A  | Pelochyta sp. JAT01       | 5.91 |
| Arctiinae sp. JAT20   | 1 | N/A  | N/A  | Delphyre flaviceps        | 6.22 |
| Arctiinae sp. JAT21+Trichromia sp. JAT04                      | 2 | 1.1  | 2.2  | Baritius acuminata        | 5.4  |
| Arctiinae sp. JAT22   | 3 | 0    | 0    | Symphlebia lophocampoides | 7.46 |
| Arctiinae sp. JAT23   | 5 | 0.56 | 1.24 | Arctiinae sp. JAT28       | 6.55 |
| Arctiinae sp. JAT24   | 3 | 0    | 0    | Leucanopsis sp. JAT03     | 4.42 |
| Arctiinae sp. JAT26   | 2 | 0    | 0    | Arctiinae sp. JAT33       | 4.78 |
| Arctiinae sp. JAT28MMZ01                                      | 1 | 0    | 0    | Arctiinae sp. JAT28       | 3    |
| Arctiinae sp. JAT28MMZ02                                      | 1 | 0    | 0    | Arctiinae sp. JAT28       | 3    |
| Arctiinae sp. JAT29   | 2 | 0    | 0    | Melese sp. JAT07          | 8.78 |
| Arctiinae sp. JAT31   | 1 | N/A  | N/A  | Machadoia xanthosticta    | 4.92 |
| Arctiinae sp. JAT32   | 4 | 1    | 1    | Leucanopsis oruba         | 3.8  |
| Arctiinae sp. JAT32+Arctiinae sp. JAT34+Leucanopsis sp. JAT02 | 5 | 1.32 | 1.8  | Arctiinae sp. JAT32MMZ01  | 4.2  |
| Arctiinae sp. JAT33   | 3 | 0    | 0    | Arctiinae sp. JAT26       | 4.78 |
| Arctiinae sp. JAT35   | 2 | 0    | 0    | Bertholdia soror          | 6.9  |
| Arctiinae sp. JAT37   | 3 | 0    | 0    | Delphyre flaviceps        | 6.77 |
| Arctiinae sp. JAT38   | 4 | 0.8  | 1.4  | Hypermaepha sp. ML01      | 6.38 |
| Arctiinae sp. JAT39   | 5 | 0.52 | 0.92 | Dinia sp. JAT01           | 6.73 |
| Argyroeides sanguinea   | 1 | N/A  | N/A  | Melese sp. JAT09          | 6.05 |
| Arhabdosia sp. ML01   | 4 | 0.83 | 1.24 | Talara sp. ML01           | 4.43 |



|  |   |      |      |                        |      |
|--|---|------|------|------------------------|------|
| Erruca hanga                                 | 4 | 0.54 | 1.08 | Mirandisca harpalyce   | 6.41 |
| Atyphopsis sp. JAT01                         | 4 | 0.26 | 0.46 | Galethalea pica        | 8.25 |
| Baritius acuminata                           | 3 | 1    | 1.6  | Pachydota affinisMMZ01 | 3.4  |
| Baritius sp. ML01                            | 3 | 0.2  | 0.2  | Baritius sp. ML01MMZ01 | 5.2  |
| Baritius sp. ML01MMZ01                       | 1 | 0    | 0    | Baritius sp. ML01      | 5    |
| Bernathonomus piperita                       | 2 | 0    | 0    | Arctiinae sp. JAT32    | 4.41 |
| Bertholdia pseudofumida                      | 3 | 0.51 | 0.77 | Bertholdia soror       | 4.75 |
| Bertholdia soror                             | 3 | 0.93 | 1.24 | Melese sp. JAT09       | 4.58 |
| Carales astur                                | 3 | 0.1  | 0.15 | Arctiinae sp. JAT31    | 5.89 |
| Carathis byblis                              | 4 | 0    | 0    | Sutonocrea reducta     | 8.27 |
| Castrica phalaenoides                        | 3 | 0.2  | 0.31 | Melese sp. JAT07       | 8.41 |
| Cissura decora                               | 5 | 0.12 | 0.31 | Bertholdia soror       | 7.06 |
| Clemensia marmorata                          | 3 | 0    | 0    | Pronola sp. ML01       | 6.73 |
| Cloesia sp. ML01                             | 7 | 0.09 | 0.31 | Illice ditrigona       | 7.05 |
| Correbidia elegansMMZ01                      | 4 | 0.35 | 0.6  | Correbidia sp. JAT01   | 3.2  |
| Correbidia elegansMMZ02+Correbidia sp. JAT01 | 6 | 0.2  | 0.2  | Correbidia elegans     | 3.2  |
| Correbidia lycoides                          | 6 | 0.27 | 0.46 | Eucereon quadricolor   | 8.93 |
| Correbidia sp. JAT02                         | 1 | N/A  | N/A  | Eucereon quadricolor   | 6.55 |
| Cosmosoma augeMMZ01                          | 1 | 0    | 0    | Cosmosoma auge         | 3.6  |
| Cosmosoma augeMMZ02                          | 2 | 0.2  | 0.4  | Cosmosoma auge         | 3.6  |
| Cosmosoma centrale                           | 6 | 0.08 | 0.15 | Mesotheren desperata   | 4.42 |
| Cosmosoma durca                              | 3 | 0.2  | 0.31 | Cosmosoma elegans      | 4.42 |
| Cosmosoma elegans                            | 4 | 0.15 | 0.31 | Cosmosoma sp. JAT02    | 2.81 |
| Cosmosoma klagesi                            | 3 | 0    | 0    | Mirandisca harpalyce   | 2.49 |
| Cosmosoma leuconoton                         | 3 | 0    | 0    | Cosmosoma plutona      | 3.13 |
| Cosmosoma plutona                            | 2 | 0.15 | 0.15 | Cosmosoma leuconoton   | 3.13 |
| Cosmosoma sp. JAT01                          | 3 | 0    | 0    | Cosmosoma elegans      | 2.83 |
| Cosmosoma sp. JAT02                          | 3 | 0    | 0    | Cosmosoma elegans      | 2.81 |
| Cosmosoma sp. JAT03                          | 1 | N/A  | N/A  | Dycladia lucetius      | 5.23 |
| Cosmosoma sp. JAT04                          | 3 | 0    | 0    | Dycladia lucetius      | 4.43 |
| Cosmosoma teuthras                           | 3 | 1.67 | 2.5  | Dycladia lucetius      | 4.74 |
| Cratoplastis catherinae                      | 3 | 0    | 0    | Viviennea moma         | 5.57 |
| Ctenucha jonesi                              | 1 | N/A  | N/A  | Galethalea pica        | 5.58 |
| Cyanopepla jucunda                           | 1 | N/A  | N/A  | Dinia sp. JAT01        | 6.41 |
| Delphyre flaviceps                           | 3 | 0.2  | 0.31 | Agylla sp. JAT14       | 5.73 |

|   |   |      |      |                          |       |
|---|---|------|------|--------------------------|-------|
| Delphyre hebes                                  | 1 | N/A  | N/A  | Galethalea pica          | 8.77  |
| Delphyre pyroperas                              | 1 | N/A  | N/A  | Galethalea pica          | 6.72  |
| Delphyre sp. ML01                               | 5 | 1.12 | 1.87 | Baritius acuminata       | 4.57  |
| Demolis albicostata                             | 1 | N/A  | N/A  | Bertholdia soror         | 8.93  |
| Dinia sp. JAT01                                 | 1 | N/A  | N/A  | Agylla sp. JAT14         | 5.39  |
| Dycladia lucetius                               | 3 | 0.1  | 0.15 | Mesothen desperata       | 3.29  |
| Dysschema amphissa                              | 5 | 1.44 | 2.4  | Dysschema sp. JAT01      | 4.2   |
| Dysschema fantasma                              | 3 | 0.1  | 0.15 | Dysschema sp. JAT01      | 4.12  |
| Dysschema hilarinaMMZ01                         | 1 | 0    | 0    | Dysschema hilarina       | 4.2   |
| Dysschema hilarinaMMZ02                         | 1 | 0    | 0    | Dysschema hilarina       | 4.2   |
| Dysschema lucifer                               | 6 | 0.34 | 0.62 | Dysschema sp. JAT01      | 5.13  |
| Dysschema neda                                  | 1 | N/A  | N/A  | Dysschema hilarina       | 6.63  |
| Dysschema sacrificia                            | 1 | N/A  | N/A  | Dysschema fantasma       | 7.81  |
| Dysschema sp. JAT01                             | 6 | 0.32 | 0.62 | Dysschema amphissa       | 3.95  |
| Dysschema subapicalis                           | 1 | N/A  | N/A  | Dysschema neda           | 7.13  |
| Echeta divisa                                   | 2 | 0.31 | 0.31 | Rhipha subflammans       | 8.29  |
| Echeta sp. JAT01                                | 2 | 0    | 0    | Baritius sp. ML01        | 10.94 |
| Elysium cingulata                               | 2 | 0.15 | 0.15 | Phaegoptera chorima      | 4.74  |
| Elysium pyrostictaMMZ01                         | 3 | 0    | 0    | Phaegoptera chorima      | 4.8   |
| Elysium pyrostictaMMZ02                         | 4 | 0    | 0    | Mazaeras francki         | 5.2   |
| Elysium superba                                 | 2 | 2.66 | 2.66 | Machadoia xanthosticta   | 6.47  |
| Epidesma sp. JAT01+Epidesma sp. JAT02           | 4 | 0.5  | 0.8  | Melese sp. JAT09         | 6     |
| Epidesma ursula                                 | 3 | 0.2  | 0.31 | Tipulodes ima            | 6.51  |
| Episcea extravagansMMZ01+Euchlaenidia transcisa | 7 | 1.8  | 2.2  | Lophocampa sp. JAT02     | 10.4  |
| Episcea extravagansMMZ02                        | 2 | 0    | 0    | Episcea extravagansMMZ03 | 9.5   |
| Episcea extravagansMMZ03                        | 1 | 0    | 0    | Episcea extravagansMMZ02 | 9.5   |
| Episcepsis endodasia                            | 4 | 0.31 | 0.62 | Delphyre flaviceps       | 6.9   |
| Episcepsis venata                               | 3 | 0.2  | 0.31 | Galethalea pica          | 5.58  |
| Erruca cardinale                                | 3 | 0.2  | 0.31 | Dycladia lucetius        | 4.75  |
| Erruca deyrollei                                | 3 | 0    | 0    | Dycladia lucetius        | 5.93  |
| Erruca sanguipuncta                             | 4 | 0.31 | 0.62 | Dycladia lucetius        | 4.26  |
| Euagra sp. JAT01                                | 1 | N/A  | N/A  | Cyanopepla jucunda       | 7.92  |
| Euagra sp. JAT02                                | 1 | N/A  | N/A  | Agylla sp. JAT14         | 6.9   |
| Eucereon apicalis                               | 4 | 0.12 | 0.32 | Agylla sp. JAT14         | 6.74  |
| Eucereon chalcodon                              | 5 | 0.83 | 1.24 | Euceriodes wernickei     | 6.07  |

|  |    |      |      |                          |       |
|--|----|------|------|--------------------------|-------|
| Eucereon discolor                          | 5  | 0.15 | 0.31 | Galethalea pica          | 8.49  |
| Eucereon griseata                          | 8  | 0.21 | 0.62 | Theages leucophaea       | 5.43  |
| Eucereon quadricolor                       | 3  | 0    | 0    | Agylla sp. JAT14         | 6.05  |
| Eucereon rosa                              | 5  | 0.12 | 0.4  | Eucereon rosaMMZ01       | 4.6   |
| Eucereon rosaMMZ01                         | 1  | 0    | 0    | Eucereon rosa            | 4.6   |
| Eucereon setosum                           | 3  | 0    | 0    | Galethalea pica          | 3.24  |
| Eucereon sp. JAT01                         | 3  | 0.1  | 0.15 | Eucereon chalcodon       | 6.73  |
| Eucereon sp. JAT02+Trichromia sp. JAT06(1) | 2  | 0    | 0    | Trichromia sp. JAT06     | 5.5   |
| Eucereon sp. JAT02+Trichromia sp. JAT06(2) | 2  | 0.4  | 0.4  | Eucereon chalcodon       | 7.7   |
| Eucereon sp. JAT03+Arctiinae sp. JAT03     | 4  | 0.45 | 0.8  | Dycladia lucetius        | 5.8   |
| Eucereon tarona                            | 3  | 0    | 0    | Galethalea pica          | 7.66  |
| Euceriodes wernickeiMMZ01                  | 1  | 0    | 0    | Euceriodes wernickei     | 7.8   |
| Euceriodes wernickeiMMZ02                  | 2  | 0    | 0    | Eucereon chalcodon       | 6.5   |
| Euceriodes wernickeiMMZ03                  | 2  | 1.6  | 1.6  | Eucereon chalcodon       | 5     |
| Eupseudosoma involutaMMZ01                 | 1  | 0    | 0    | Hyperandra appendiculata | 6.3   |
| Eupseudosoma involutaMMZ02                 | 2  | 0    | 0    | Baritius acuminata       | 8.6   |
| Euthyone purpurea                          | 1  | N/A  | N/A  | Tricypha sp. JAT01       | 10.15 |
| Galethalea pica                            | 3  | 0.21 | 0.32 | Eucereon setosum         | 3.24  |
| Grapheia paramarmorea                      | 2  | 0.77 | 0.77 | Baritius sp. ML01        | 6.91  |
| Haemanota bicolor                          | 1  | N/A  | N/A  | Trichromia sp. JAT05     | 8.41  |
| Heterodontia haematica                     | 6  | 0.05 | 0.15 | Dycladia lucetius        | 6.56  |
| Holophaea erharda                          | 3  | 0    | 0    | Ichoria tricincta        | 7.41  |
| Hyaleucerea vulnerata                      | 5  | 0.21 | 0.46 | Arctiinae sp. JAT02      | 6.56  |
| Hyalurga fenestrata                        | 5  | 0.15 | 0.31 | Hyalurga sp. JAT01       | 8.31  |
| Hyalurga sp. JAT01                         | 2  | 0    | 0    | Pelochyta sp. JAT01      | 6.21  |
| Hyperandra appendiculata                   | 4  | 0    | 0    | Eupseudosoma involuta    | 6.89  |
| Hypercompe sp. JAT01                       | 4  | 0    | 0    | Machadoia xanthosticta   | 9.04  |
| Hypermaepha sp. ML01                       | 13 | 0.07 | 0.46 | Lycomorphodes sp. ML01   | 6.23  |
| Hypidalia enervis                          | 2  | 0    | 0    | Eupseudosoma involuta    | 7.9   |
| Ichoria chalcomedusa                       | 4  | 0    | 0    | Pelochyta sp. JAT01      | 6.38  |
| Ichoria tricincta                          | 2  | 0.64 | 1.25 | Rhynchopyga meisteri     | 6.22  |
| Idalus agastus+Idalus sp. JAT01            | 4  | 0    | 0    | Idalus sp. JAT01         | 6.1   |
| Idalus agastusMMZ01                        | 2  | 1    | 1    | Idalus sp. JAT01MMZ01    | 8     |
| Idalus agastusMMZ02                        | 2  | 0    | 0    | Idalus sp. JAT01MMZ01    | 6.8   |
| Idalus lineosusMMZ01                       | 5  | 0.2  | 0.2  | Ormetica rothschildi     | 7.5   |
| Idalus lineosusMMZ02                       | 8  | 0.1  | 0.2  | Idalus lineosus          | 3     |

|   |   |      |      |                              |       |
|---|---|------|------|------------------------------|-------|
| Idalus lineosusMMZ03                        | 1 | 0    | 0    | Idalus lineosus              | 3     |
| Idalus sp. JAT01                            | 6 | 1.4  | 1.4  | Idalus sp. JAT01MMZ01        | 6.7   |
| Illice brunea                               | 2 | 0.2  | 0.2  | Stenognatha gentilis         | 7.1   |
| Illice brunea+Illice sp. ML01               | 6 | 0.36 | 0.6  | Pachydota affinisMMZ03       | 6.7   |
| Illice cryptopygra                          | 2 | 0.16 | 0.16 | Baritius acuminata           | 6.26  |
| Illice ditrigona                            | 5 | 0.22 | 0.49 | Illice sp. ML05              | 6.38  |
| Illice endoxantha                           | 8 | 0.17 | 0.46 | Illice sp. ML04              | 3.93  |
| Illice sp. ML02                             | 3 | N/A  | N/A  | Illice sp. ML03              | 10.68 |
| Illice sp. ML03                             | 1 | N/A  | N/A  | Baritius acuminata           | 9.62  |
| Illice sp. ML04MMZ01                        | 1 | 0    | 0    | Illice sp. ML04              | 3.8   |
| Illice sp. ML04MMZ02                        | 3 | 1.2  | 2    | Illice endoxantha            | 4.2   |
| Illice sp. ML05                             | 2 | 0    | 0    | Illice ditrigona             | 6.38  |
| Isanthrene incendiaria                      | 2 | 0.17 | 0.17 | Dycladia lucetius            | 8.29  |
| Ischnocampa lugubrisMMZ01                   | 2 | 0    | 0    | Ischnocampa lugubris         | 3.8   |
| Ischnocampa lugubrisMMZ02                   | 4 | 0.05 | 0.2  | Ischnocampa lugubris         | 3.8   |
| Ischnognatha leucapera                      | 3 | 0    | 0    | Rhynchopyga meisteri         | 8.57  |
| Isia alcumena                               | 3 | 0.2  | 0.31 | Illice sp. ML05              | 9.46  |
| Lepidokirbyia vittipes                      | 3 | 0.1  | 0.15 | Ormetica iheringi            | 8.42  |
| Lepidozikania sp. JAT01                     | 4 | 0.23 | 0.46 | Agylla sp. JAT14             | 6.41  |
| Leucanopsis coniota                         | 3 | 0.2  | 0.31 | Arctiinae sp. JAT32          | 3.95  |
| Leucanopsis leucanina                       | 2 | 1.55 | 1.55 | Leucanopsis sp. JAT07        | 4.77  |
| Leucanopsis mandus                          | 4 | 0    | 0    | Arctiinae sp. JAT32          | 3.93  |
| Leucanopsis oruba                           | 3 | 0    | 0    | Arctiinae sp. JAT32          | 3.31  |
| Leucanopsis sp. JAT01                       | 5 | 0.09 | 0.15 | Arctiinae sp. JAT32          | 4.75  |
| Leucanopsis sp. JAT03                       | 5 | 0.3  | 0.62 | Arctiinae sp. JAT28          | 3.29  |
| Leucanopsis sp. JAT04+Arctiinae sp. JAT25   | 6 | 0    | 0    | Cosmosoma elegans            | 9.9   |
| Leucanopsis sp. JAT04+Leucanopsis sp. JAT06 | 3 | 0.4  | 0.4  | Arctiinae sp. JAT27MMZ01     | 2     |
| Leucanopsis sp. JAT05                       | 3 | 0.2  | 0.31 | Baritius acuminata           | 5.23  |
| Leucanopsis sp. JAT07                       | 4 | 0    | 0    | Arctiinae sp. JAT27          | 4.43  |
| Leucanopsis sp. JAT08+Arctiinae sp. JAT18   | 5 | 0.96 | 1.2  | Leucanopsis sp. JAT01        | 5     |
| Lophocampa arpi                             | 2 | 0.15 | 0.15 | Opharus notata               | 4.27  |
| Lophocampa sp. JAT01MMZ01                   | 3 | 0.2  | 0.2  | Lophocampa sp.<br>JAT01MMZ02 | 4.8   |
| Lophocampa sp. JAT01MMZ02                   | 1 | 0    | 0    | Lophocampa texta             | 3.8   |
| Lophocampa sp. JAT02MMZ01                   | 1 | 0    | 0    | Lophocampa textaMMZ01        | 4.6   |
| Lophocampa sp. JAT02MMZ02                   | 3 | 1.86 | 2.8  | Lophocampa sp. JAT02         | 5     |

|  |    |      |      |   |      |
|--|----|------|------|---|------|
| Lophocampa texta                                     | 5  | 0.4  | 0.4  | Lophocampa textaMMZ01                             | 3.4  |
| Lophocampa textaMMZ01                                | 1  | 0    | 0    | Lophocampa texta                                  | 3.4  |
| Lycomorphodes sp. ML01+Lycomorphodes strigosa        | 5  | 0.52 | 0.8  | Hypermaepha sp. ML01                              | 6.5  |
| Machadoia xanthostictaMMZ01                          | 3  | 0.46 | 0.8  | Psychopasma erosa                                 | 5    |
| Machadoia xanthostictaMMZ02                          | 1  | 0    | 0    | Phaegoptera histrionica                           | 3.8  |
| Macrocneme sp. JAT01                                 | 4  | 0.3  | 0.6  | Macrocneme sp. JAT01                              | 2.6  |
| Macrocneme sp. JAT01MMZ02                            | 1  | 0    | 0    | Macrocneme sp. JAT01                              | 3    |
| Macrocneme sp. JAT01xx                               | 1  | 0    | 0    | Macrocneme sp. JAT01                              | 3    |
| Macrocneme sp. JAT03                                 | 1  | 0    | 0    | Macrocneme sp. JAT01                              | 4.4  |
| Mazaeras francki                                     | 5  | 0.18 | 0.46 | Opharus notata                                    | 5.73 |
| Melese castrena+Melese sp. JAT08                     | 15 | 0.74 | 1    | Melese incertus+Melese sp. JAT06+Melese sp. JAT12 | 3.4  |
| Melese castrena+Melese sp. JAT10                     | 11 | 0.2  | 0.4  | Melese sp. JAT07+Melese sp. JAT10                 | 3.4  |
| Melese chozeba                                       | 9  | 0.31 | 1.4  | Bertholdia soror                                  | 5.23 |
| Melese incertus+Melese sp. JAT06+Melese sp. JAT12    | 12 | 0.11 | 0.4  | Melese castrena+Melese sp. JAT08                  | 3.4  |
| Melese incertusMMZ                                   | 3  | 0    | 0    | Melese castrena+Melese sp. JAT10                  | 6.9  |
| Melese sp. JAT01+Melese sp. JAT03                    | 21 | 0.22 | 1.4  | Melese castrena+Melese sp. JAT08                  | 4.2  |
| Melese sp. JAT02                                     | 6  | 0.34 | 0.77 | Melese sp. JAT09                                  | 6.34 |
| Melese sp. JAT04+Melese sp. JAT11                    | 6  | 0.06 | 0.2  | Melese sp. JAT09                                  | 6.7  |
| Melese sp. JAT05                                     | 7  | 0.26 | 0.77 | Melese sp. JAT07                                  | 7.9  |
| Melese sp. JAT07+Melese sp. JAT10(dimorfismo sexual) | 24 | 0.47 | 0.8  | Melese castrena sp08                              | 3.2  |
| Melese sp. JAT09                                     | 5  | 0.38 | 0.8  | Bertholdia soror                                  | 4.58 |
| Mesothen desperataMMZ01                              | 4  | 0.2  | 0.2  | Dycladia lucetius                                 | 3.2  |
| Mesothen desperataMMZ02                              | 3  | 0    | 0    | Cosmosoma plutona                                 | 4    |
| Metalobosia diaxantha                                | 3  | 1    | 1    | Metalobosia diaxanthaMMZ01                        | 5.6  |
| Metalobosia diaxanthaMMZ01                           | 1  | 0    | 0    | Metalobosia diaxantha                             | 5.6  |
| Mirandisca harpalyce                                 | 4  | 0.08 | 0.15 | Cosmosoma klagesi                                 | 2.49 |
| Napata sp. JAT01                                     | 2  | 0.15 | 0.15 | Galethalea pica                                   | 5.75 |
| Neidalia dulcicula                                   | 1  | N/A  | N/A  | Leucanopsis leucanina                             | 10.7 |

|  |   |      |      |                         |       |
|--|---|------|------|-------------------------|-------|
| Neonerita dorsipuncta                      | 3 | 0.1  | 0.15 | Lepidokirbyia vittipes  | 10.88 |
| Neotrichura nigripes                       | 4 | 0.08 | 0.15 | Melese sp. JAT09        | 6.32  |
| Nodozana coresaMMZ01                       | 1 | 0    | 0    | Aclytia jonesi          | 7.3   |
| Nodozana coresaMMZ02                       | 2 | 0.2  | 0.2  | Leucanopsis sp. JAT04   | 6.9   |
| Nyridela chalciope                         | 1 | N/A  | N/A  | Mesothen desperata      | 6.56  |
| Ochrodota pronapides                       | 6 | 0.07 | 0.16 | Baritius acuminata      | 5.39  |
| Opharus basalis                            | 3 | 0    | 0    | Pachydota affinis       | 5.06  |
| Opharus brasiliensis                       | 4 | 0    | 0    | Phaegoptera chorima     | 6.05  |
| Opharus notata                             | 3 | 0.1  | 0.15 | Lophocampa arpi         | 4.27  |
| Opharus procroides                         | 3 | 0    | 0    | Opharus brasiliensis    | 6.95  |
| Opharus rema                               | 3 | 0    | 0    | Arctiidae sp. JAT16     | 7.22  |
| Ormetica iheringi                          | 3 | 0    | 0    | Ormetica rothschildi    | 4.27  |
| Ormetica rothschildi                       | 4 | 0    | 0    | Ormetica iheringi       | 4.27  |
| Pachydota affinisMMZ01                     | 1 | 0    | 0    | Baritius acuminata      | 3.2   |
| Pachydota affinisMMZ02                     | 2 | 0    | 0    | Pachydota affinisMMZ01  | 3.8   |
| Pachydota affinisMMZ03                     | 3 | 0.02 | 0.2  | Baritius acuminata      | 4.2   |
| Paracles fuscaMMZ01                        | 3 | 0    | 0    | Paracles fusca          | 5.9   |
| Paracles fuscaMMZ02                        | 1 | 0    | 0    | Paracles sp. JAT02      | 6.8   |
| Paracles fuscaMMZ03                        | 3 | 0.4  | 0.4  | Paracles sp. JAT03      | 5.4   |
| Paracles sp. JAT01                         | 1 | N/A  | N/A  | Paracles sp. JAT03      | 6.58  |
| Paracles sp. JAT02                         | 2 | 0    | 0    | Paracles sp. JAT01      | 7.25  |
| Paracles sp. JAT03                         | 1 | N/A  | N/A  | Paracles sp. JAT01      | 6.58  |
| Paracles sp. JAT04                         | 1 | N/A  | N/A  | Paracles fusca          | 6.12  |
| Paracles variegata                         | 3 | 0    | 0    | Paracles sp. JAT03      | 8.29  |
| Pareuchaetes sp. ML01                      | 3 | 0    | 0    | Pelochyta sp. JAT01     | 7.73  |
| Pelochyta cinereaMMZ01                     | 1 | 0    | 0    | Pelochyta cinerea       | 5.2   |
| Pelochyta cinereaMMZ02                     | 3 | 0.13 | 0.2  | Baritius acuminata      | 4.2   |
| Pelochyta sp. JAT01                        | 3 | 0.31 | 0.46 | Arctiinae sp. JAT28     | 4.25  |
| Phaegoptera chorima                        | 7 | 0.22 | 0.46 | Arctiidae sp. JAT16     | 2.66  |
| Phaegoptera fuscaMMZ001                    | 6 | 0.93 | 1.8  | Phaegoptera chorima     | 3     |
| Phaegoptera fuscaMMZ02+Pachydota sp. JAT01 | 2 | 0.4  | 0.4  | Phaegoptera histrionica | 2.2   |
| Phaegoptera histrionica                    | 5 | 0.3  | 0.8  | Phaegoptera fusca       | 2.2   |
| Philoros affinis                           | 2 | 0.15 | 0.15 | Galethalea pica         | 6.76  |
| Phoenicoprocta haemorrhoidalis             | 2 | 0    | 0    | Sychesia dryas          | 8.58  |
| Poliopastea indistinctaMMZ01               | 4 | 0.85 | 1.2  | Cosmosoma plutona       | 6.9   |
| Poliopastea indistinctaMMZ02               | 1 | 0    | 0    | Agylla sp. JAT14        | 6.3   |

|  |    |      |      |                           |      |
|--|----|------|------|---------------------------|------|
| Praepiella sesapina  | 1  | N/A  | N/A  | Pelochyta sp. JAT01       | 9.27 |
| Pronola sp. ML01   | 5  | 0.28 | 0.46 | Clemensia marmorata       | 6.73 |
| Pseudosphex rubripalpus  | 3  | 0    | 0    | Baritius acuminata        | 8.6  |
| Psilopleura sanguipuncta                                       | 8  | 0.31 | 0.61 | Dycladia lucetius         | 4.09 |
| Psychopasma erosa  | 1  | N/A  | N/A  | Phaegoptera chorima       | 5.07 |
| Rhabdatomis sp. ML01   | 3  | 0    | 0    | Lophocampa sp. JAT01      | 8.45 |
| Rhipha flavithorax   | 2  | 0    | 0    | Ormetica rothschildi      | 6.22 |
| Rhipha subflammans   | 2  | 0    | 0    | Baritius acuminata        | 6.38 |
| Rhynchopyga meisteri   | 4  | 0.3  | 0.51 | Opharus basalis           | 5.96 |
| Robinsonia spitzi  | 3  | 0.1  | 0.15 | Melese sp. JAT09          | 8.07 |
| Romualdia elongata   | 1  | N/A  | N/A  | Opharus notata            | 5.32 |
| Sarosa sp. ML01  | 3  | 0    | 0    | Dycladia lucetius         | 4.67 |
| Saurita sp. JAT01+Arctiinae sp. JAT07                          | 5  | 0    | 0    | Mesothera desperata       | 4.2  |
| Scaptius sp. ML01  | 3  | 0.1  | 0.15 | Viviennea moma            | 8.94 |
| Sciopsyche tropica   | 1  | N/A  | N/A  | Leucanopsis leucanina     | 7.39 |
| Selenarctia elissa   | 2  | 0    | 0    | Ormetica iheringi         | 5.07 |
| Stenognatha gentilis   | 5  | 0.37 | 0.77 | Baritius acuminata        | 6.55 |
| Sutonocrea reducta   | 1  | N/A  | N/A  | Ormetica rothschildi      | 6.38 |
| Sychesia dryas   | 4  | 0.08 | 0.15 | Arctiidae sp. JAT16       | 4.41 |
| Symphlebia distincta+Symphlebia sp. JAT02                      | 7  | 0    | 0    | Arctiinae sp. JAT22       | 6.7  |
| Symphlebia distinctaMMZ01                                      | 1  | 0    | 0    | Arctiinae sp. JAT22       | 7.6  |
| Symphlebia lophocampoides                                      | 3  | 0    | 0    | Arctiinae sp. JAT22       | 7.46 |
| Symphlebia perflua+Arctiinae sp. JAT30                         | 7  | 0    | 0    | Symphlebia lophocampoides | 8.2  |
| Talara semiflava   | 4  | 0.28 | 0.46 | Pachydota affinis         | 6.22 |
| Talara sp. ML01  | 6  | 0.08 | 0.16 | Arhabdosia sp. ML01       | 4.43 |
| Theages leucophaeaMMZ01  | 2  | 1    | 2    | Eucereon griseata         | 5.5  |
| Theages leucophaeaMMZ02  | 2  | 0    | 0    | Eucereon griseata         | 4.8  |
| Thysanoprymna pyrrhopyga                                       | 4  | 0    | 0    | Pachydota affinis         | 6.93 |
| Tipulodes ima  | 1  | N/A  | N/A  | Napata sp. JAT01          | 6.18 |
| Trichromia sp. JAT01+Trichromia sp. JAT02+Trichormia sp. JAT03 | 10 | 0.2  | 0.2  | Aclytia jonesi            | 9    |
| Trichromia sp. JAT01+Trichromia sp. JAT02+Trichormia sp. JAT04 | 14 | 0.64 | 1    | Melese sp. JAT07          | 6.7  |
| Trichromia sp. JAT05   | 10 | 0.66 | 1.39 | Arctiinae sp. JAT28       | 6.55 |
| Trichromia sp. JAT06   | 5  | 0    | 0    | Eucereon sp. JAT02MMZ01   | 5.5  |
| Tricypha imperialis  | 3  | 0.31 | 0.46 | Pelochyta sp. JAT01       | 6.56 |

|                     |   |      |      |                        |      |
|---------------------|---|------|------|------------------------|------|
| Tricypha sp. JAT01  | 2 | 0    | 0    | Baritius acuminata     | 4.9  |
| Virbia divisaMMZ01  | 7 | 0.02 | 0.2  | Virbia divisa          | 5.4  |
| Virbia divisaMMZ02  | 5 | 0    | 0    | Virbia divisa          | 5.4  |
| Viviennea dolens    | 2 | 1.86 | 1.86 | Ormetica iheringi      | 7.4  |
| Viviennea moma      | 3 | 0    | 0    | Viviennea superba      | 5.09 |
| Viviennea superba   | 1 | N/A  | N/A  | Viviennea moma         | 5.09 |
| Xanthophaeina levis | 2 | 0    | 0    | Machadoia xanthosticta | 5.44 |